Run on:

Title:

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U32828 Haemophilus
AE006127 Pasteurel
AE004313 Vibrio ch
U17642 Haemophilus
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AF163661 Salmonell
AF163662 Salmonell
AE013955 Yersinia
AJ414144 Yersinia
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-MODEL-frame+p2n.model.-DEV-xlp
-MODEL-frame+p2n.model.-DEV-xlp
-MODEL-frame+p2n.model.-DEV-xlp
-MODEL-frame+p2n.model.-DEV-xlp
-MODEL-frame+p2n.model.-DEV-xlp
-MOSTOLIGNS-DEVEXT-0.model.-DEVEXT-0
-MOSTOLIGNS-DEVEXT-0.model.-DEVEXT-0
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-USER-US09912020_@CGN_1_1.3637_@FUNAL_25112002_091428_24247 -NCPU-6 -ICPU-3
-NO_XIPXY -NO_MANP -LARGEORERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPOP-10 -FGAPOP-6 -FGAPEXT-7
-YGAPOP-10 -YGAPOP-10 - DELEXT-7
                                                                                             November 26, 2002, 10:19:57 ; Search time 3268 Seconds (without alignments) 4247.870 Million cell updates/sec
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1 MKVTLPEFERAGVMVVGDVM......FEDGCSTTNIIKKIQQDKKG 477
            GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

    nucleic search, using frame_plus_p2n model

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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Maximum DB seq length: 200000000
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Sequence Caulobact Campyloba Mesorhizo Helicobac

AE006022 AL139077 AP003000 AE001509

Pseudomon

Seguence

AX374740

Helicobac

Buchnera

Buchnera

Neisseria Neisseria Neisseria Neisseria Ralstonia Burkholde Streptomy Fusobacte Aquifex a

AL646061 AF159428

Sequence

AX044030

Sequence

Streptomy

AL035478 AE010481 AF210249

AE000696

Sequence

AX363670 Sequence AE000387 Escherich

AX189075 Sequence

Description

AE005534 Escherich AP002564 Escherich

Salmonel] Salmonell

AF155126 AE008847

Escherichia

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220 99 240

200 009 260 780 280 840 300 900 320 096

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PAT 15-FEB-2002
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GEVLVLNNEDGCGSTTNIIKKIQODKKG"
gEVLVLNNEDGCGSTTNIIKKIQODKKG"
          08-AUG-2001
                                                                                    subdivision; Enterobacteriaceae;
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            linear
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Forsyth, R.A., Ohlsen, K.L. and Zyskind, J.W.
Genes identified as required for proliferation
Patent: Wo O148210-9A 276 05-JUL-2001:
Elitra Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Conservative:
Mismatches:
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       AX189075 Sequence 276 from Patent AX189075
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                              781
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Conservative:
Mismatches:
Indels:
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352 c 447 g 3
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Escherichia.
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Escherichia coli
Sequence 165
AX363670
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Query Match:
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Blatther, F.R., Plunkett, G. III, Bloch, C.A., Perna, N.T., Burland, V., Riley, N., Collado-Vides, J., Glasner, J.D., Rode, C.K., Mayhew, G.F., Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A., Rose, D.J., The complete genome sequence of Escherichia coli K-12
Schence 277 (5331), 1453-1474 (1997)
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Direct Submission
Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics,
                                                                                                                                                                                                                                                                                                                                        1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gamma subdivision; Enterobacterlaceae;
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Escherichia coli K12 MG1655 section 277 of 400 of the complete
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GluGluAlaCysPhePheAlaAsnAlaAlaAlaGlyValValValGlyLysLeuGlyThr
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Escherichia coli K12
Bacteria; Proteobacteria;
Escherichia.
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AE000387.1 GI:1789431
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us-09-912-020-325.p2n.rge

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                                                                                                                              modification"
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/note="REP (
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Direct Submission

Submitted (13-OCT-1998) Laboratory of Genetics, University of Walsconsin, 445 Henry Mall, Madison, WI 53706, USA

Walsconsin, 445 Henry Mall, Madison, WI 53706, USA

This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by Will grants HG00301 and HG01428 (from the Human Genome Project and NCHGR). The entire sequence was independently readed frames were determined using GeneMark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 3032 (e-mall: mark@amber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (http://www.genetics.udu). Annotation of the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli Genome Project's World Wide Web site

(http://www.genetics.wisc.edu). *** The E. coli K12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein or RNA-encoding) are now designated as gene synonyms instead of labels. This should allow them to be searched for in Entez as gene
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ARKRGEKVVMTNGVFDILHAGHVSYLANARKLGDRLIVAVNSDASTKRLKGDSRPVNP
LEQRMIVLGALEAVDWVVSFEEDTPQRLIAGILPDLLVKGGDYKPEEIAGSKEVWANG
GEVLVLNFEDGCSTINIIKKIQODKKG"
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TITKLRVLSRNQQLIRLDFEBGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASV
QOMIQLARKAGVPVLIDPKGTDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMK
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                                                                                                                                              Direct Submission
Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
608-263-7459
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/note="factor Sigma70; predicted +1 start at 3194409"
complement(1721, .4561)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .11307
/organism="Escherichia coli K12"
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/db_xref="GI:1789432"
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complement(240. 1673)
/gene="b3052"
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/note="b3053"
                                                                                   3 (bases 1 to 11307)
Blattner, F.R.
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                                                                                                                                                                                                                                                                                                                                 Plunkett, G. III
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SYTAMPEMETEELESOPPOADEWOHYAARUNESTELESESSARSTITESDEVON
SYTAMPEMETEELESOPPOADEWOHYAARUNESTELDHOOFFTRAMOGEALRIELILIGM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPNGELPADLASRVQPLFSTDFYREKWLVAVDGSQIETALDQGEVKAGEFAEPICELE
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COMpLAGNET (5878 . . 5902)
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1 REP sequence"
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/bound_molety="Fur predicted site"
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/note="central position to predicted promoter: -38.5"
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/note="factor Sigma70; predicted +1 start at 3198820"
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                                                                              'note="f946; 99 pct identical (1 gap) to GLNE_ECOLI
/function="enzyme; Proteins - translation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="No predicted promoter"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALQELPGHVSEDCFTAERELVRASWQKWLVEE" complement(4584. .5885)
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/gene="ygiF"
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6747. 6775
/note="factor sigma70; predicted +1 start at 3199503"
/gene="cca"
/note="cca"
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6811. 8049
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                                                                                                                                                                                                              /note="0412; 100 pct identical to CCA_ECOLI SW: P06961; Site No. 933"
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Mismatches:
Indels:
Gaps:
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Escherichia coli K-12 genome; approximately 68 minutes
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PAKWHPEIDTGIHTLMTLSWAAMLSPQVDVRFATLCHDLGKGLTPPELWPRHHGHGPA
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Submitted (01-JUN-1995) Guy Plunkett, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
On Feb 27, 1996 this sequence version replaced gi:882576.
This sequence was determined as part of the E. coli Genome Project
(Frederick R. Blattner, director) at the University of
Wisconsin-Madison. Supported by award HG00301 from the NIH Human
Genome Project. The entire sequence was independently determined
from E. coli MG1655; overlaps with other sequence determinations
are annotated. The end of this entry overlaps the start of the
entry ECOWAG7 (U18997) by 1596 bp. This entry should be considered
somewhat provisional; it will be updated and merged with others at
                              Proteobacteria; gamma subdivision; Enterobacteriaceae;
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1. .25638
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/gene="cca"
6686. .7924
/gene="cca"
                                                                                     (bases 1 to 25638)
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Escherichia.
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200 949 220 889 240 829 260 769 280 709 300 649 320 589 340 529 360 469 380 409 400 349 420

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PheGluGluGlyBheGluGlyValAspProGlnProLeuHisGluArgIleAsnGlnAla
                                                                                                                                                                      GCTTCTCTCGGTGCTAATGCACGCCTGGTCGGGTTGACGGGCATTGACGATGCAGCGCGC
                                                                                                                                     TTTGAAGAAGGTTTCGAAGGTGTTGATCCGCAGCCGCTGCACGAGCGGATTAATCAGGCG
                                                                                                                                                                                                                                                                                                                                             AlaaspTyrGluLeuSerAlaLeuLeuValThrArgSerGluGlnGlyMetSerLeuLeu
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                                                                                                                                                                                                                                                                                                                                                                                          GlnProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspValThr
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                            /translation-*MKPSTEWMRYLAPLAVIAIIALLPVPAGLENHTWLYFAVFTGVI
VGIILEPVPGAVVAAVGISIIAILSPWLLFSPEQDAQPGFKETAKSLSWAVSGFSNSV
ULLFAAFBWFGTGYFKTGLGRRIALLILVKKMGHRTFLELGYAVFSELLILAVTPSNSA
RGAGIIYPIIRNLPPLYOSQOPUSSSSIGSYIMWMGIVACVTSAIFLTAAVADNLLL
IGLMKSASHATLSWGDWFLGMLPLSILLVLLVPWLAYVLYPPVLKSGDQVPRWAETEL
                                                                                                                                                                                                    /traislation-"MEVIOIETSCDETGIAIYDDEKGLLANQLYSQVKLHADYGGVVP
ELASRDHVRKTVPLIQAALKESGLTAKDIDAVAYTAGPGLVGALLVGATVGRSLAFAW
POYAIPWHAEGHLLAPMLEDNPPEEPFYALLVSGGHTQLISYTGIGGYEELGGESIDD
AVATEWHAEGHLLAPMGEPLLSKWAAGTAGRFVFPRPWTDRPGLDFSGIKTPA
ANTIRNGTDDQTRADIPARAEDAVVDTLMKCKRALDGTGFKRLDFSSGLKTFA
ANTIRNGTDDQTRANIPARECTDNGAMIAYAGWYRFKAGATADLGVSVRPKWPLAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                   /LTADSlation="MPVIKVRENEPPDVALRRFKRSCEKAGVLAEVRREFYEKPTTE
RKRAKASAVKRHAKKLARENARRTRLY"
                                                                                     QAMGPLCSREKRALGLAVGALVLWIFGGDYIDAAWVGYSVALMLLLEXISWDDIVSN
KAANNVFFWLASLITLATGLNNTGFISWFGKLLAGSLSGYSPTWVWALIVVFYLLRY
FFASATAYTSALAPMATAAALAMPETPLPVFCLMVGAAIGLGSILTPYATGPSPIYYG
SGYLPTADYWRLGAIFGLIFLVLLVITGLLWMPVVLL"
complement (14325. .15338)
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No. 847; alternate gen
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Matches:
Conservative:
Mismatches:
Indels:
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         /protein_id="AAA89143.1"
/db_xref="GI:882586"
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/db_xref="G1:882587"
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/transl_table=11
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/transl_table=11
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                                                                                                                                                                                                                                                                                  14862. .19917
/note="similar to
(ECORPSRPO)"
1576 .15791
/gene="rpsu"
15576. .15791
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/note="CG Site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="dnaG"
15902. 174.
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2393.00
100.00%
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                                                                                                                                                                                                                                                                                                                                                                  /note="CG
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Best Local Similarity:
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DB:
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/transl_table=11
/product="glycogen biosynthesis, rpoS dependent"
/product="glycogen biosynthesis, rpoS dependent"
/pprotein_id="AAGS8183.1"
/db_xref="GI:12517625"
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                                                              /protein_id="AAG58180.1"
/db_xref="GI:12517622"
/translation="MFIAWYWIVLIVLVVVGYFLHLKRYCRAFRQDRDALLEARNKYL
NSTREETAEKVE"
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/transl_table=11
/product="3,4 dihydroxy-2-butanone-4-phosphate synthase"
/product="3,4 dihydroxy-2-butanone-4-phosphate synthase"
/protein_id="Anof58181.1"
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FPAETWITVEQNALTIRHGSGIVCLCITEDRRKOLDLPMWYENNTSAYGTGFTVTIEDA
EGVTFGVSAADRITTYRAALAGGRKESBLNRFCHVFPIERAQAGGVLTRGGHTEDATIBL
MTLAGFKPAGGVLCELTNDDGTWARAPECIEFANKHNMALVTIEDLVAYRQAHERKAS"
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/gene="24400"
/function="orf; Unknown function"
/note="Residues 1 to 106 of 111 are 86.79 pct identical to residues 9 to 114 of 116 from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="putative enzyme; Not classified"
/note="Residues 1 to 204 of 204 are 99.01 pct identical to
residues 1 to 204 of 209 from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAG58182.1" ·
/bc.xref="G1:12517624"
/translation="WALNIYOYEETIMIDPKKIEQIARQVHESWPKGIREFGEDVEKK
IRQTLQAQLTRLDLVSREEFDVQTQVLLRTREKLAL/LEQRSSELEARNNSVADLQSPP
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/note="O-island #124; Region of the EDL933 chromosome not
homologous to E. coli K-12 MG1655"
complement(2713. .2919)
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/function="putative enzyme; Macromolecule synthesis,
modification: Polysaccharides - (cytoplasmic)"
/note="Residues 3 to 68 of 68 are 98.48 pct identical to
residues 1 to 66 of 66 from Escherichia coli K-12 Strain
MG1655: B3049"
                                                                                                                                                                                                                                                                                                                                                                                          /note="Residues 1 to 217 of 217 are 100.00 pct identical to residues 1 to 217 of 217 from Escherichia coli K-12 strain MG1655: B3041"
                                                                                                                                                                                                                                                                                                                                           function="enzyme; Biosynthesis of cofactors, carriers:
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/protein_id="AAG58184.1"
/note="No significant matches"
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/transl_table=11
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/gene="24402"
3182. .3796
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/gene="24400"
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/gene="24402"
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/function="orf; Unknown function"
/note="Residues 1 to 257 of 257 are 100.00 pct identical
to residues 1 to 257 of 257 from Escherichia coli K-12
Strain MG1655: B3 04 0"
Strain MG1655: B3 04 0"
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/transl_table=11
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/db_xref="G1:12517621"
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KSIKRATILITIGISHNFPGGIATFVTASSNLEIGEGTALAVALHNIPEGLAVAGPV
YAATGSKRRAILMAGISGIAELIGGVLAMLIGSRIEPVWAAIMAAVAGIMVALSVD
ELMPLAKEIDPNNNPSYGUCGMSVMGFSLVLLQTAGIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E 2 (bases 1 to 12088)
S Perra,N.T., Plunkett,G. III, Burland,V., Mau,B., Glasner,J.D.,
Rose,D.J., Mayhew,G.F., Evans,P.S., Gregor,J., Kirkpatrick,H.A.,
Rose,D.J., Mayhew,G.F., Boutin,A., Shao,Y., Miller,L.,
Grotbeck,E.J., Davis,N.W., Lim,A., Dimalanta,E., Potamousis,K.,
Apodaca,J., Anantharaman,T.S., Lin,J., Yen,G., Schwartz,D.C.,
Welch,R.A. and Blattner,F.R.
Direct Submission
Lose ton (22-ocr-2000) Laboratory of Genetics, University of
Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
Location/Qualifiers
I. 12088 Maisconsin, Beschrichia coli 0157:H7 EDL933"
//strain="Boolean"
                                                                                                                                                                                                                                                                                                                   AE005534 12088 bp. DNA linear BCT 21-MAR-2001 Escherichia coli 0157:H7 EDL933 genome, contig 3 of 3, section 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 12088)
Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shoo, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R.
Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7
Nature, 409 (6819), 529-533 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli 0157:H7 EDL933.
Escherichia coli 0157:H7 EDL933
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                           228 GCCGGGAGTAAAGAAGTCTGGGCCAACGGTGGCGAAGTGTTGGTGCTCAACTTTGAAGAC 169
                             441 AlaGlySerLysGluValTrpAlaAsnGlyGlyĞluValLeuValLeuAsnPheGluAsp
                                                                                                                                           /gene="Z4398"
/function="orf; Unknown function"
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complement(920. .1090)
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AE005534 AE005174
AE005534.1 GI:12517620
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/note="24397"
89. .862
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VERSION
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JOURNAL
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AUTHORS
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JOURNAL
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gene

FEATURES

CDS

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REFERENCE AUTHORS

KEYWORDS

SOURCE

PUBMED

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(1-477) x AE005534 (1-12088)
  US-09-912-020-325
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                                                                                                                                                          /translation-"MILFADYNTPYLFAISFVLLIGLLEIFALICGHMLSGALDAHLD
WYDSITTGHESQALHYLNIGRLPALVVLCLLAGFFGLIGLLAHCINYWQSFLSNLF
WYPYSLLFTIAVHYTGKIYAPWIPRDHSSALTEEEYIGSMALITGHQATSGNPCEGK
LTDHFGQIHYLLLEPEEGKIFTKGDKVLIICRLSATRYLAENNP
                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="z440s"
/function="putative enzyme: Not classified"
/function="putative enzyme: Not classified"
//functe="Residues" to 477 of 477 are 99.58 pct identical to
residues 1 to 477 of 477 from Escherichia coli K-12 Strain
MG1655: B3052"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /traislation-*mkyteperracymygdymldrywygdsrisperpydykyn
Tierrpgaanyamiaslganariugletgtegdydyngrygdsstabapyrykyn
Tierrpgaanyamiaslganariuglegdegydyngrisdyargalasy
Tyrkirvlsrnoolirldergegyddoppiherinoalssigalusbyrargalasy
OQMIOLARKAGYPULIDPRGTDFERYRGATLITPNISEFRAVGRKTEEELYBRGM
LIADYELSALLVTRSEQGMSLLQPGRAPLHMPTQAQEVYDVTGAGDYIGVLAATLAA
GNSLERACFRANAAGYVOKLGTSTYSPIELENAYRGRADTGFGYWTEEELKLAVYA
ARRGEKVWTNGYPDIHAGHVSYLANARKLGDRLIVAVNSDASTRRLKGDSRPVND
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                                                                                                /function="putative membrane; Not classified"
//note="Residues 1 to 553 of 553 are 98.73 pct identical to
residues 1 to 553 of 553 from Escherichia coli K-12 Strain
MG1655: B0051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pct identical to coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function="enzyme; Macromolecule synthesis, modification:
Proteins - translation and modification"
/note="Residues 1 to 946 of 946 are 98.73 pct identical to
residues 1 to 946 of 946 from Escherichia coli K-12 Strain
MG1655: B3053"
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Mismatches:
Indels:
Gaps:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative kinase"
/protein_id="AAG58186.1"
/db_xref="G1:12517628"
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                                                3838. .5499
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3838. .5499
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                                                                                                                                                   /codon_start=
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2385.00
99.79%
99.58%
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Best Local Similarity:
Query Match:
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                                                 AlaSerLeuGlyAlaAsnAlaArgLeuValGlyLeuThrGlyIleAspAspAlaAlaArg
                                                                                                                                                                                                          GlyValMetThrGluGluGluLeuLySLeuAlaValAlaAlaAlaArgLySArgGlyGlu
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MetLysValThrLeuProGluPheGluArgAlaGlyValMetValValGlyAspValMet
                                                                                                                                                                                                                                                                                        AlaAspTyrGluLeuSerAlaLeuLeuValThrArgSerGluGlnGlyMetSerLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCGTGATGACCGAAGAGGBAACTGAAGCTGGCTGTAGTGGCAGCGCGTAAACGTGGTGAA
                         LeuAspArgTyrTrpTyrGlyProThrSerArglleSerProGluAlaProValProVal
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/translation-*MOCOMERVDIYGERFRTRASQLFPGLRAVASYINEHREVVLDQ
TAMBIAATLNTSDATVIRALQALGFAGLRDLKRTLEQMLGPALSSEKMSTTYSNLTS
DYNTALDFVLEGHLYTCNVLSEPENHRALAQAVALLVQARQVAIFGIGASGILADYTA
RLFRRIGLFATALMTTGIGLAGOLTALQRGOVLIMAGKSAHREGITTLERARKGIP
VILLTNALDSRFSKDASIVIHVPRGDEKGKTPLHGTVLCLEMIVWSVASAVPQRAVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
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DPSKPVGSGGLVOGKYMLGSTWNAPMEAPFERDOFFHGVGVDVFTRRANGFTRR
DPSKRYGSGGLVOGKYMLSLTWNAPMEAFFERDOFFHGVGVDGVYLPFHKANGFLGM
EPLPTFIANDVIKMPDVPRYTEEYRKHLVEIFG"
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DCAAGVSFQSMAPDSIVMIEQMESIAHLEAHLQTPHMKAYSEAVKGDVLEMNIRILQP
                                                                                                                                                       Hayashi,T.
Direct Submission
Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Genome
Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Genome
Information Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871,
Japan (E-mall:kenégen-info.osaka-u.ac.jp,
URL:http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365,
Fax:81-6-6879-2047)
                                                                                                         5 (bases 1 to 307962)
Ohnishi,M., Kurokawa,K., Makino,K., Yasunaga,T., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [ gi|1789406 percent identity
E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to YGIN_ECOLI gi|1789407 percent identity
100 in 104 aa (Conserved in E.coli K-12)"
/codon_start=1
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/note="probable transcriptional regulator, similar to regulators (Rpik family) e.g. [Bacillus subtilis]

gill 8248807|emb|CAB93068.1| percent identity 25 in 236
/codon_start=1
Complete genome sequence of enterohemorrhagic Escherichia coli 0.157:H7 and genomic comparison: with a laboratory strain K-12 DNA Res. 8 (1), 11-22 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative transcriptional regulator"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to MDAB_ECOLI
100 in 193 aa (Conserved in F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="0157:H7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:83334"
72. .653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="GI:13363384"
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684. .998
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72. .653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /qene="ECs3910"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="ECs3912"
                                                                                                      (bases 1 to 307962)
                                                                                                                                                                                                                                                                                                                                            genome project.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete nucleotide sequence of the prophage VT2-Sakai carrying the verofcoxin 2 genes of the enterohemorrhagic Escherichia coli 0157:H7 derived from the Sakai outbreak derived from the Sakai outbreak Genes Genet. Syst. 74 (5), 227-239 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAR-2001
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Ohnishi,M., Murata,T., Nakayama,K., Kuhara,S., Hattori,M.,
Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli 0157:H7 (strain:0157:H7, sub_strain:RIMD 0509952)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Comparative analysis of the whole set of rRNA operons between an enterohemorrhagic Escherichia coli 0157:H7 Sakai strain and an Escherichia coli K-12 strain MG1655 Syst. Appl. Microbiol. 23 (3), 315-324 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 (sites)
Yokoyama,K., Makino,K., Kubota,Y., Watanabe,M., Kimura,S.,
Yutsudo,C.H., Kurokawa,K., Ishii,K., Hattori,M., Abe,H., Iida,T.
Yamamoto,K., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (sites)
Makino,K., Yokoyama,K., Kubota,Y., Yutsudo,C.H., Kimura,S.,
Kurokawa,K., Ishii,K., Hattori,M., Tatsuno,I., Abe,H., Lida,T.,
Yamamoto,K., Ohnishi,M., Hayashi,T., Yasunaga,T., Honda,T.,
Sasakawa,C. and Shinagawa,H.
                                                                                                                                                                                                                                                           6347
                                                                                                         6587
                                                                                                                                                                                     6706 AAAGTGGTAATGACCAACGGTGTCTTCGATATCCTACATGCCGGGCACGTCTCTTATCTG 6647
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Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T.,
Tanaka,M., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C.,
Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and
Shinagawa,H.
                                                                                                                                                          400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         460
                                                      361 AlaAsnAlaArgLysLeuGlyAspArgLeuIleValAlaValAsnSerAspAlaSerThr 380
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, complete genome, section 15/20
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                                                                                 6646 GCAAATGCCCGCAAGCTGGGTGACCGCTTGATTGTTGCCGTCAACAGCGATGCTCCACC
                                                                                                                                                          LysArgLeuLysGlyAspSerArgProValAsnProLeuGluGlnArgMetIleValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         441 AlaGlySerLysGluValTrpAlaAsnGlyGlyGluValLeuValLeuAsnPheGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6346 GGTTGCTCGACCACTAACATTATCAAGAAGATCCAACAGGATAAAAAAGGC 6296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             461 GlyCysSerThrThrAsnIleIleLysLysIleGlnGlnAspLysLysGly 477
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AP002564 BA000007
AP002564.1 GI:13363382
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system ATP-binding protein"

/db_xref="d1:1339.1"

/db_xref="d1:1339.39.1"

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AQKTPYILLDEPTTMLDLRYQVEILELHDLTRHCKFVVVVLHDLRFAVNYGDTLLF

LRQGKVVRVLNEGEHCTPELVKAVFDVDVHASINFLTGKPFFMPFRGVEKV"
iron-siderophore transport
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24442 ACCGATTTTGAGGGCTACCGGGGGGCTACGCTGTTAACGCCGAATCTCTCGGAATTTGAA
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                                                                                                                                                                                                                              Conservative:
Mismatches:
/product="putative ABC-type
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/protein_id="BAB37336_1"
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LERRYQAQINALKATLDEDADFVFATWRGDTGKRYDGWCGRLDGGAL
SIPEGGRMDVSAERTLEELDADFVFATWRGDTGKRQDELAAMEKVNPGWCGPFIPAGR
GRYVLISREFAISNGFASLGAMAAQIQSQIAGRPLPEAK"
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ANEDHWYINELPRIAAALLTGASLGAVGALLQAYIRNPLGEPHIGLAGAALAV
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TAAILILDEQTLLANRTWLAGDLAGQDWATLGTSAWFSLGGVVLAIYLAPSLNMLALG
IPMAAGGLGVSVLRTRFTLATALLGGAAVSTAGFTGTSAWFSLGGVVLAIYLAPSLNMLALG
IPLSACVGALLLLLAIALLCGAAVSTAGFTGFTCHTPHELATGVWTALVGAPVTRHFKLVSADLRVL
COMPIEMENT (4911. 5720)
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           /note="probable ferrichrome-binding protein, similar to ferrichrome-binding proteins e.g. [Bacillus subtilis] g1|585132|sp|P37580|FHUD_BACSU percent identity 27 in 220
                                                                                                                                                                                                                                                                                                                                                                                                                            in
                                                                                                                                                                                                                                                                                                                                                                                       (permease), similar to ferrichrome ABC transporter (permease) e.g. [Bacillus subtilis] gil706797|sp|P49937|FHUG_BACSU percent identity 33
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complement(4911. 5720)
/gene="ECs3916"
/note="probable ABC-type iron-siderophore transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ferrichrome ABC
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/gene="ECS3914"
complement(2885...3934)
/gene="ECS3914"
/note="probable ferrichrome ABC transporter
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transporter"
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transporter"
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/db_xref="GI:13363388"
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/codon_start=1
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                                                                                 24143
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                         400
                                                    320
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                      AlaAsnAlaArgLysLeuGlyAspArgLeuIleValAlaValAsnSerAspAlaSerThr
                                                                                                                                                                                                                                                                 AlaGlySerLysGluValTrpAlaAsnGlyGlyGluValLeuValLeuAsnPheGluAsp
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Jin,U.-H., Chung,T.-W. and Kim,C.-H.
Direct Submission
Submitted (28-MAY-1999) Oriental Medicine,
Sukjang-Dong 707, Kyungju 780-714, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .1431
/organism="Salmonella typhimurium"
/db_xref="taxon:602"
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Jin,U.-H., Chung,T.-W. and Kim,C.-H.
ADP-heptose synthase (rfaE) gene of
Unpublished
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/note="WaaE"
1. .>1431
/gene="rfaE"
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TveerpggaanvamniaslganarlygltgiddaaralskTlaevnvkcdpvsvpthp
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TTTKLRVLSRNODLIRLDFERGFEGVDPQPLHERINGALGSTGALVLSDYAKGALTSV
TTTKLRVLSRNODLIRLDFERFRGATLTPNLSFERAVGKCSEDELVERGMK
LIADYDLSALLVTSROGWTLDPRKTDFFRYRGHTLTPNLSFERAVGKCSEDELVERGMK
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GNTLEFACYFANAAAGVVVGKLGTSTVSPIELENAVRGRADTGFGVWTEEELRQAVAS
ARKRGEKVWMTWGVFDILLAGHTSYLNARKGDRLIAGNTSRPVNP
LEQRMIVLGALESVDWVVSFEDDTPGRLIAGILDDLLVKGGDYRPEEIAGSEBVWN
GEGWWLIAFEDGCTFNIIKKIOTESEK"

357 c 467 g 296 t
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447
1.9
10
0
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Matches:
Conservative:
Mismatches:
Indels:
                           /product="ADP-heptose synthase"
/protein_id="AAK20933.1"
/db_xref="GI:13383336"
                                                                                                                                                                                                                                                                                                                                             (1-1431)
                                                                                                                                                                                                                                                                                                                    Gaps:
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                             US-09-912-020-325 (1-477) x AF155126
                                                                                                                                                                                                                                                 1.95e-131
2276.00
97.90%
93.91%
95.11%
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Best Local Similarity:
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ReguonDB;
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AUTHORS
                      TITLE
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220 of the complete
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Latreille, P., Courtney, L., Porwollik, S., Åli, J., Dante, M., Du, F.,
Hou, S., Layman, D., Leonard, S., Nauyen, C., Scott, K., Holmes, A.,
Grewal, N., Mulvaney, E., Ryan, E., Sun, H., Florea, L., Miller, W.,
Stoneking, T., Nhan, M., Waterston, R. and Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gamma subdivision; Enterobacteriaceae;
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                        260
                                             780
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                                                                  1081 GCGAACGCGCGCAAACTGGGCGGACCGCCTGATTGTTGCGGTCAATAGTGACGCCTCGACT
                                                                                                                                                                                                                                                                                                                                                  LysArgLeuLysGlyAspSerArgProValAsnProLeuGluGlnArgMetIleValLeu
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                                                                                                                                                                                                                                                                                                     AlaAsnAlaArgLysLeuGlyAspArgLeuIleValAlaValAsnSerAspAlaSerThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    441 AlaGlySerLysGluValTrpAlaAsnGlyGlyGluValLeuValLeuAsnPheGluAsp
                      GlnProGlyLysAlaProLeuHisMetProThrGinAlaGlnGluValTyrAspValThr
                                    LysValValMetThrAsnGlyValPheAspIleLeuHisAlaGlyHisValSerTyrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyCysSerThrThrAsnIleIleLysLysIleGlnGlnAspLysLys 476
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LT2, section 151 of
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AE008847.1 GI:16421751
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1 (bases 1 to 20604)
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AE008847/c
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MTLAGFRPAGVLCETTNDDGFWARAPECIAFAGGHNMAVVTIEDLVAYRQAHERKAS
complement(778...783)
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Location/Qualifiers
                                                                                                                                                                                                                                                Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs; GLIMMER; http://www.tigr.org/softlab/glimmer/glimmer.html and GeneMark; http://opal.biology.gatech.edu/GeneMark/
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Blastp hit to AAC76077.1 (217 aa), 96% identity in aa 1
217"
                                                                                                                                                                                                                                                                                                                                                                                                            EC numbers were kindly provided by Junko Yabuzaki and the Kyoto Encyclopedia of Genes and Genomes; http://www.genome.ad.jp/kegg/, and Pedro Romero and Peter Karp at EcoCyc; http://ecocyc.PangeaSystems.com/ecocyc/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The analyses of ribosome binding sites and promoter binding sites were kindly provided by Heladia Salgado, Julio Collado-Vides and
                                                                                                      Department of , 4444 Forest
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1139. .1505
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1146. 11505
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                                                                                                      Center, De
Medicine,
                                                                                            Submitted (29-MAR-2001) Genome Sequencing Center
Genetics, Washington University School of Medicin
Park Boulevard, St. Louis, MO 63108, USA
COMMENT Supported by NIH grant 50 01 A143283
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2 (bases 1 to 20604)
The Salmonella typhimurium Genome Sequencing
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="LT2"
complement(116. .783)
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gene

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                                                                                                                                                                                                                                                                                                                                                                         QTMISLARQAGVPVLIDPKGTDFERYRGÄTLLTPNLSEFEAVAGKCKSEDELVERGMK
LIADYDLSALLVTRSEQGMTLLQPNKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAA
GNTLEEACYFANAAAGVVVGKLGTSTVSPIELENAVRGRADTGFGVMTEEELRQAVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARKRGEKVVMTNGVFDILHAGHVSYLANARKLGDRLIVAVNSDASTKRLKGESRPVNP
LEQRMIVLGALESVDWVVSFEEDTPQRLIAGILPDJLVKGGDYKPEEIAGSEEVWANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coli
                                                                     /nole="bifunctional; similar to E. coli putative kinase (AAC76088.1); Blastp hit to AAC76088.1 (477 aa), 93% identity in aa 1 - 476"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="putative RBS for rfaE; RegulonDB:STMS1H003231" complement(6305. .9163)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="glnE"
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/note="regulates P-II (GlnB) and GlnK; similar to E. (adenylylating enzyme for glutamine synthetase (AAC76089.1); Blastp hit to AAC76089.1 (946 aa), 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 LeuSerSerIleGlyAlaLeuValLeuSerAspTyrAlaLysGlyAlaLeuAlaSerVal 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09
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      MetLysValThrLeuDroGluPheGluArgAlaGlyValMetValValClyAspValMet

      |||||||||

      |||||||||

      ArgaaagtaaarctGcCagcGTTTGAaCGTGCAGGCGTCATGGTTGTGGGTGATGTAATG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6017 GCGCTGAGCAAAACGCTGGCGGAGGTCAATGTGAAGTGCGACTTCGTTTCTGTGCCGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HisProThrIleThrLysLeuArgValLeuSerArgAsnGlnGlnLeuIleArgLeuAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 ValLysValAsnThrIleGluGluArgProGlyGlyAlaAlaAsnValAlaMetAsnIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AlaSerLeuGlyAlaAsnAlaArgLeuValGlyLeuThrGlyIleAspASaAlaAlaArg
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445
19
12
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEVMVLNFEDGCSTINIIKKIQTESEK' complement(6264. .6269)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-912-020-325 (1-477) x AE008847 (1-20604)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(6305. .9148)
complement(4824. .6257)
                                                                                                                                                                          /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="STM3201"
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2265.00
97.48%
93.49%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="rfaE"
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product-"putative inner membrane protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product-"putative membrane protein"
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VQCVQNTVAEDLSKNGLELESVSLTNFNQTSKEHFNPNNAFDAEGLIKLTQETERRRR
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ERHREAEGTRILAERQIOGTEIERRÇAVRSKKVEARREVRIKEIEĞQGVTETANĞTKS
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                                                                                                                                                                                                 /note="similar to E. coli glycogen biosynthesis, rpoS dependent (AAC76085.1); Blastp hit to AAC76085.1 (66 aa), 78% identity in aa 2 - 66"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="putative RBS for STM3198; RegulonDB:STMS1H003229"
2046. .2666
                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2671. 4364
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/note="yqik"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="putative RBS for glgS; RegulonDB:STMSIH003228" complement(1885. 1905)
/note="putative binding site for CRP, RegulonDB: STMSIH000051"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to E. coli putative oxidoreductase (AAC76086.1); Blastp hit to AAC76086.1 (209 aa), 72% identity in aa 1 - 201"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anote-"similar to E. coli putative membrane protein (AAC76087.1); Blastp hit to AAC76087.1 (553 aa), 928 identity in aa 1 - 553"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(4824. .6269)
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/note="STM3200"
                                                                        complement(1579. .1797)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /bound_moiety="CRP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="STM3198"
2033, 2039
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gene

RBS

CDS

gene

RBS

CDS

gene

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VLDATTILVDARQQLANARYTYLINGLNIKYAALGILAEQDLLALNSTLGKPIPTSPES
                                                                               E 1 (bases 1 to 258050)

Salmonella.

Salmonella.

Salmonella.

Brkhill, J., Dougan, G., James, K.D., Thomson, N.R., Pickard, D., Waln, J., Churcher, C., Mungall, K.L., Bentley, S.D., Holden, M.T.G., Sebaihia, M., Baker, S., Basham, D., Brooks, K., Chillingworth, T., Connerton, P., Cronin, A., Davis, P., Davies, R.M., Dowd, L., Mhite, N., Farrar, J., Feltwell, T., Handlin, N., Haque, A., Hien, T. T., Holroyd, S., Jagels, K., Krogh, A., Larsen, T.S., Leather, S., Moule, S., O'Gaora, P., Parry, C., Quall, M., Rutherford, K., Simmonds, M., Skelton, J., Stevens, K., Whitehead, S. and Barrell, B.G.

Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18

L. Nature 413 (6888), 848-852 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Orthologue of E. coli ygiB (YGIB_ECOLI); Fasta hit to YGIB_ECOLI (234 aa), 97% identity in 223 aa overlap. Contains a possible N-terminal signal sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /genew.CYY3364"
/note="SIMilar to Salmonella enteritidis outer membrane
/note="Similar to Salmonella enteritidis outer membrane
protein Tolc precursor tolc SW:TOLC_SALEN (054001) (491
aa) fasta scores: E(): 0, 99.0% id in 491 aa, and to
Escherichia coli outer membrane protein tolc precursor
tolc or match or muka or refi SW:TOLC_ECOLI (P02930) (495
aa) fasta scores: E(): 0, 89.7% id in 495 aa
Orthologue of E. coli tolc (TOLC_ECOLI); Fasta hit to
TOLC_ECOLI (495 aa), 90% identity in 495 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      available
                               Salmonella enterica subsp. enterica serovar Typhi.
Salmonella enterica subsp. enterica serovar Typhi
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Salmonella enterica subsp. enterica serovar
Typhi"
                                                                                                                                                                                                                                                                                                                                                                                Submitted (25-OCT-2001) Submitted on behalf of the Salmonalla sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Details of S. typhi sequencing at the Sanger Centre to the World Wide Web.
(URL, http://www.sanger.ac.uk/Projects/S_typhi/).
Location/Qualifiers
1. .258050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref-"taxon:90370"
                                                                                                                                                                                                                                                                                                                                                                                                                                       E-mail: parkhill@sanger.ac.uk
Notes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="STY3364"
/note="tolC"
69. .1544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1757. .2428
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1757. .2428
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Parkhill,J.
Direct Submission
 AL627278.1
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REFERENCE
AUTHORS
TITLE
JOURNAL
                                                    ORGANISM
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                                                                                                    REFERENCE
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 VERSION
KEYWORDS
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                                                                                                                                                                                                                                                    TITLE
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                                 SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                     GlyAlaGlyAspThrVallleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeu 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlyvalMetThrGluGluGluLeuLysLeuAlavalAlaAlaAlaArgLysArgGlyGlu 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaAsnAlaArgLysLeuGlyAspArgLeuIleValAlaValAsnSerAspAlaSerThr 380
                                                                                                                                                                                                                                                                                                                      GlnProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspValThr 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlnGlnMetIleGlnLeuAlaArgLysAlaGlyValProValLeuIleAspProLysGly
                                                                      AlaAspTyrGluLeuSerAlaLeuLeuValThrArgSerGluGlnGlyMetSerLeuLeu
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/translation="MFDQYRKTILAGAVALTCGLTAASTFAAGFQPAQPAGKLGAVVV 
PPYGNAPLTALVELDSHIDSVYVYHGKGEKGVYYYYVDSTVGRSLETVDGIPTFGLYQ 
KPRANNYTETRAVELDSHIDSVYVYHGKGEKGVYYYYVDSTSLQTKYTKVAPGFEDRLY 
LVNTHTFTPQGAEFHWHGEKDKNAGILDAGPAGGALPFDIAPYTFVVDTGGEYRWWLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QDTFYNGHDMNINKRGYLMGIRETPRGTFTAVQCQHWYEFDMMGQILADHKLPRGFLD
ARBESIETWOGGYLLRVGKRDKREDGOTHWHTHOQIIEDWGSGRVVDWDLYKLIDP
MRDALLGALDAGAVCWVDLAHAGQOAKLEPDTFYGDALGYGAGRRMAHWYD
DDSIILSSRHQGIVKIGRDKQVKWILAPSKGWNKQLASKLLKPVDDHGKPLTCDENGK
CKDTDPDFYTYDHTAWLSSKGTHLTVPDMGDGRCH.BQPALPTMKYSRFYEKKIDEKKGT
VQQVWERGKERGYDFYSPITSVVEQKORDPNFGCFGGSINLFDVGKFTVGKLDDKK
TKEVKVEIDVLSDKFNQTHTRALLVHPTQMFK
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IAKDKAAGISLFDAKSQFKKAKFAMYTAYHDKKERWSDGKDPAAFIKTGLDAAGMSQA
DFEAALKDPAVQETLEKWKAAYDVAKIQGVPAYVVNGKYLIYTKNIKSIDSMAELVRE
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/note="62Y3371"
/gene="STY3371"
/note="Similar to Enterobacter amnigenus disulfide
isomerase dabA TR:09XDP1 (EMB::AF(12826) (222 aa) fasta
.~~~: E(): 0, 90.1% id in 222 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Similar to Klebsiella pneumoniae arylsulfate
sulfotransferase assT TR:P97036 (EMBL:U32616) (598 aa)
fasta scores: E(): 0, 86.8% id in 598 aa"
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                                                                                                                                                                                                                                                                                                             /product="probable arylsulfate sulfotransferase"
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oxidoreductase, score 12.90, E-value
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Mismatches:
                                                                                                                                                                                                                                                                                                                                         /protein_id="CAD07717.1"
/db_xref="GI:16504269"
/db_xref="SPTREMBL:0823N6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="SPTREMBL:Q8Z3N5"
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/product="disulfide isome
/protein_id="CAD07718:1"
/db_xref="GI:16504270"
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/gene="STY3371"
/note="Pfam match to
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/gene="STY3372"
/note="dsbB"
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/gene="STY3371"
                                                                      6004. .7800
/gene="STY3370"
       /gene="STY3370"
                                      'note="assT"
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Best Local Similarity:
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//transl_table=11
/product="conserved hypothetical protein"
/product="conserved hypothetical protein"
/product="conserved hypothetical protein"
/protein_id="CAD07714.1"
/protein_id=
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GSTKRTAILLTIGTSLHNPPEGIATFVTASSNLELGFGIALAVALHNIPEGLAVAGPV
STATGSKRTAILLTIGTSLHNPPEGIATFVTASSNLELGFGIALAVALHNIPEGLAVAGPV
STATGSKRTPTFWAGISGMAETIGGVLAWLILGSLVSPIVMAAIMAAVAGIMVALSVD
ELMPLAKEIDPNNNPSYGVLGGMSIMGLSLVILQTIGIG"
6004. .7800
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FPDHENLLPAYFAEDEHPPWDKYVVKPIFSREGANVSIIENGKTIESVEGPYGEEGMI
VQQFYPLPKFGDSYTLIGSWLINDQPAGIGIREDRALITQDLSRFYPHIFVEG"
complement (3659. .4489)
/gene="STY3367"
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/product="conserved hypothetical protein"
/protein_id="CaD07715.1"
/bc.xref="fg1:16504287"
/db_xref="SPTERME.:0873N7"
/translation="WVMLTKCLSCKDNIMSLTCMPALFLGGGSPMNVLDDNDYTRAWR
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AQRLVELLAPVPVALDKEAMGFDHGSWGVLIKMYPNADIPWYQLSVDSTKPAAWHFEM
GRKLATLRDEGVMLVASGWYVNINLEYVBWHGDNI PYPWAASFNDFVKANLTWGGPVEO
HPLWYKLQHGGGALSNPTPBEHFLLLVLGARDGKEPTITPVDGIEBMSSISMLSSVQVG
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/translation="MSVPLILTLAGAATFIGAFLGVLGQKPSNRVLAFSLGFAAGIM
                                                                                                                                                                        /translation="MKRTKSIHHASFRKSWSARHLTPVALAVTAVFMLAGCEKSDETV
                                                                                                                                                                                                    SLYQNADDCSAANPGKSAECTTAYNNALKEAERTAPKYATREDCVAEFGEGQCQQAPA
QAGMAPENQAQAQQSSGSFWMPLMAGYMMGRLMGGGAGFAQQPLFSSKNPASPAYGKY
                                                                                                                                                                                                                                                                          !DAAGKNYGAAQPGRTMTVPKTAMAPKPATTTTVTRGGFGESVAKQSTMQRSAAGTST
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Contains multiple possible membrane spanning hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Orthologue of E. coli ygiD (YGID_ECOLI); Fasta hit
to YGID_ECOLI (271 aa), 87% identity in 266 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in
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                                                                                                                                                                                                                                                                                                                                                                         /gene="STY3365"
/note="PS00013 Prokaryotic membrane lipoprotein lipid
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overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Orthologue of E. colinygic (YGIC_ECOLI); Fasta YGIC_ECOLI (386 aa), 94% identity in 386 aa ove
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                            /product="possible lipoprotein"
/protein_id="CaD07713.1"
/db_xref="GI:16504265"
                                                                                                                                 /db_xref="SPTREMBL:Q8XGZ1"
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/db_xref="GI:16504268"
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/gene="STY3367"
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/transl_table=11
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/gene="STY3368"
4588. .5361
/gene="STY3368"
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/transl_table=11
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2434. .3597
/gene="STY3366"
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/gene="STY3366"
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AlaGlySerLysGluValTrpAlaAsnGlyGlyGluValLeuValLeuAsnPheGluAsp
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GCGGGCAGCGAAGAGTCTGGGCCAACGCGGGGAAGTCATGGTGCTGAACTTCGAAGAT
1. .1476
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LOCUS
DEFINITION
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VERSION
KEYWORDS
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LEQRAIVLGALESVDWVSFEEDTPQRLIAGILPDLLVKGGDYKPEELAGSEEVWANG
GEVNAVLNFEDGCSTTNIIKKIQTESEK"
                                                                                                                                    BCT 12-JAN-2000
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Valvano, M.A., Marolda, C.L., Bittner, M., Glaskin-Clay, M., Simon, T.L. and Klena, J.D.
The ries gene from Escherichia coli encodes a bifunctional protein involved in biosynthesis of the lipopolysaccharide core precursor
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Submitted (28-JUN-1999) Micorbiology and Immunology, University
Western Ontario, DSB3003, London, Ontario NGASC1, Canada
Location/Qualifiers
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gene, complete cds
GlyCysSerThrThrAsnIleIleLysLysIleGlnGlnAspLysLys 476
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of ADP-glyceromannoheptose"
/note="putative ADP transferase"
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J. Bacteriol. 182 (2), 488-497 (2000)
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AF163661
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Valvano, M.A.
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Salmonella enterica
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Pred. No. Score: Percent S Best Loca Query Mat	: Similarity: al Similarity: ctch:	8.03e-130 2250.00 97.06% 92.86% 94.02%	Length: Matches: Conservative: Mismatches: Indels: Gaps:	1476 442 20 114 0	
US-09-912	-020-325 (1-47	7) x AF163661 (1-1476)		
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Qy 21 Db 61	LeuAspArgTyrT: 	rpTyrGlyProThrS 	erArgileSerProG 	luAlaProValProVal 	40
Oy 41 Db 121	ValLysValAs 	nThrlleGluGluArgP ::: TACCGTTGAGGAACGCC	roGlyGlyAlaAla 	AsnValAlaMetAsnIle 	60 180
Oy 61 Db 181	AlaSerLeuGly 	aAsnAlaArgLeu 	ValGlyLeuThrGlyll(leAspAspAlaAlaArg 	80 240
Qy 81 Db 241	Alai GCGC	LeuAlaAspVa ::: TGGCGGAGGT	.lasnvallysCysaspPhe 	heValSerValProThr TCGTTTCTGTGCCGACG	100 300
Oy 101 Db 301	HisProThrlleThrLys 	LeuArg	yvalLeuSerArgAsnGlnG 	AsnGlnGlnLeuIleArgLeuAsp 	120 360
Oy 121 Db 361		yvalAs CGTGGA	pProGlnProLeuHisGluArg 	luArgIleAsnGlnAla 	140 420
Qy 141 Db 421	LeuSerSerIleGl	lyalaLeuvalLeuserA 	erAspTyrAlaLysGly 	lyAlaLeuAlaSerVal GCGCTCTGACCAGCGTG	160 480
Oy 161 Db 481		nLeuAlaArgLy :: CTGGCGCGCA	sAlaGlyvalProvalL :	illeuileaspProLysGly 	180 540
Oy 181 Db 541	ThraspPheGluarg	Tyrar TACCG	9GlyAlaThrLeuLeuThrProA 	coAsnLeuSerGluPheGlu 	200
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Qy 221 Db 661	AlaAspTyr GCTGATTAC	GluLeuSerAlaLeuLeuValThrArg: :::	alThrargSerGluGlnG 	.lnGlyMetSerLeuLeu aGGGAATGACGCTGCTG	240 720
Qy 241 Db 721	. GlnProGlyLysAlaP caaccGaaTaaaGCGC	laProLeuHisMetF 	ProLeuHisMetProThrGlnalaGlnGluValTyraspV. 	luValTyrAspValThr 	260 780
Qy 261 Db 781	G1y GGT	hrVallleGlyVall 	AlaGlyAspThrVallleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsn. 	laAlaGlyAsnSerLeu 	280 840
Qy 281 Db 841	GluGluAlaCy 	hePheAlaAsnAlaA ::: ATTTCGCCAATGCGG	SPhePheAlaAsnAlaAlaAlaGlyValValValGlyLySLeur :::	alGlyLysLeuGlyThr 	300
Qy 301 Db 901	ω — E₁	rolleGluLeuGluA 	erthrvalSerProlleGluLeuGluAsnalavalArgGlyArgAlaAspThr 	rgAlaAspThrGlyPhe :ccccGGATACCGGCTTC	320 960

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AF163662 1464 bp DNA linear BCT 12-JAN-2000 Salmonella enterica RfaE mutant (rfaE) gene. rfaE-543 allele, complete cds.
AF163662.1 GI:5734095
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Salmonella enterica
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Bandonella.

1 (bases 1 to 1464)
Valvano,M.A., Marolda,C.L., Bittner,M., Glaskin-Clay,M., Simon,T.L.
and Klena,J.D.
The riag gene from Escherichia coli encodes a bifunctional protein
involved in biosynthesis of the lipopolysaccharide core precursor
ADP-L-glycero-D-manno-heptose
J. Bacteriol. 182 (2), 488-497 (2000)
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1. 1464
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                                                                                                                                                                                                                          GlyAlaLeuGluAlaValAspTrpValValSerPheGluGluAspThrProGlnArgLeu 420
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Valvano, M.A.
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Deng,W., Burland,V., Plunkett,G. III, Boutin,A., Mayhew,G.F.
Liss,P., Perna,N.T., Rose,D.J., Mau,B., Zhou,S., Schwartz,D., Fetherston,J.D., Lindler,L.E., Brubaker,R.R., Plana,G.V., Straley,S.C., McDonough,K.A., Nilles,M.L., Matson,J.S., Genome Sequence of Yersinia pestis KIM
J. Bacteriol. 184 (16), 4601-4611 (2002)
                                                                                                                                                                                                                321 GlyvalMetThrGluGluGluLeuLysLeuAlaValAlaAlaAlaArgLysArgGlyGlu
                                                                                                                                                                                                                                                        361 AlaAsnAlaArgLysLeuGlyAspArgLeuIleValAlaValAsnSerAspAlaSerThr
    GCGGTCGCGGGAAATGTAAAAGCGAAGACGAACTGGTTGAACGCCGCATGAAACTCATT
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Yersinia pestis KIM
Bacteria, Proteobacteria,
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EKKVWTWGSPDILHAGHYSTLANARKLGDRLIVANWSDASTKRLKGESRRYNBLEOR

MIVLGALESVDWVGSFEEDTPQRLIAGILPDLLVKGGDYKPEEIAGSEEVWANGGEWW

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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                /gene="rfaE"
/note="deletion of
                                                                                                 /gene="rfaE"
/note="glycine t
/replace="g"
818^819
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DB:
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Best Local
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VVKVDTIEEREGGAANVAMIASLGANARLVGLTGIDDAAAALICKLSEVRYRCDBYS
VPTHTTKLRVLSRNQOLIRLDFEEGFDGVDPTPIFERIQLALPQIGALVLSDYAKG
ALNSVQPMIQLARKANVPVLLDPRGSDFERYRGATLLFPNLSEFEAVVGRCKNEEELV
NRGMQLVADFELSALVYTRSEQGMTLLQLGRPFLHLPTQAREVFDVTGGTDYIGYLA
AALAGNGSLESCFLANAAAGVVVGRLGTSYVSPTELENAIRGREFTGGWUBGQLK
INAQAARGYGRXVVWTNGIPDILHAGHYSYLANARKLGEBR
RPVNFLEQRMVVLGALEAVDWVVPFEEDTFQRLIADILVAGGDYRPHIAGSEE
                                                           /note="residues 1 to 77 of 93 are 90.90 pct identical to residues 21 to 97 of 116 from E. coli K12: B3042; residues 1 to 82 of 93 are 89.02 pct identical to residues 13 to 94 of 111 from GenPept: >9b|A658182.1|AE005534) 24400 gene product [Escherichia coli 0157:H7
                                                                                                                                                                                                                                                                  /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function="putative transport"
/note="residues 3 to 413 of 418 are 70.07 pct identical to
residues 1 to 411 of 418 from E. coli K12 : B4141"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
/product="adenylylating enzyme for glutamine synthetase"
/protein_id="aAM87073.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of 481 are 86.10 pct identical to from E. coli K12 : B3052"
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RRRVWVRIAWSQVLQTSGTAETLQOLSTLAESMIIAARDWLYQVCCRELGTPCNRQGV
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complement(6121, 9003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative kinase"
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/db_xref="G1:21960486"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="residues 6 to 480 residues 1 to 475 of 477 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(4556..6001)
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complement(4556..6001)
/gene="y3524"
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VASGNVVHNRLGKWQGESSPYPWAESFNQFVRDNLSYQGDDHPLVNFWQHEGAALSN
PSPEHTLPLLYVLGSWGKEPVSIPTDGYEMGSLSMLSVQIG"
complement(1441. .2094)
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FVWTNAPHLEIYRCISPADTVTLSSHPDYNRRPRNYTCSADLYLALLDKRNNWSARGLL
HHRRDYIVAIQFTAGGDFHPALRISPWTIALLIHLGNYQNAELNLASRGLYNOHRALY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product-"3,4 dihydroxy-2-butanone-4-phosphate synthase"

*protein_id="AAM87068.1"

/db_xref="GI:21960482"

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EGVTTGVSAADRLTIIRKAIADNAKPADLNRPGHVFPLRGQPGGVLSRRGHTEASIDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complement (234. .1016)
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/gene="y3519"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="ribb"
/function="enzyme; biosynthesis of cofactors, carriers:
                          2 (bases 1 to 10641)
Deng,W., Burland,V., Plunkett,G: III, Boutin,A., Mayhew,G.F.,
Liss,P., Perna,N.T., Rose,D.J., Mau,B., Zhou,S., Schwartz,D.C.
Fetherston,J.D., Lindler,L.E., Brubaker,R.R., Plana,G.V.,
Straley,S.C., McDonough,K.A., Nilles,M.L., Matson,J.S.,
Blattner,F.R. and Perry,R.D.
Direct Submission
Submitted (21-FEB-2002) Genetics, University of Wisconsin, 445
Henry Mall, Madison, WI 53706, USA
                                                                                                                                                                                                                                                                                                                                         /organism="Yersinia pestis KIM"
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POPLLICAMCKIGGGELNFSSDIDLIFAYPENGOTOGGGRRELDNAQFFTRLGORLIKA
LODHTIGGFYRYNWHIGHEFOSSPILOLISAALLENDYOGGGRREFRAMMINGGA
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LOATADGGTOTELNDELUNGRAMMINGGATALENDHOWNERVERDILGGETP
LOATADGGTOTELNDELUNGRAMMINGGATALENDHOWNERVERDILGGETP
GGEDSEHGETKSLAMMANSTLAENDHOWNERVERDILGGETP
GGEDSEHGETKSLAMMANSTLAENDHOWNERVERDILGGETP
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RUCKSASPWASGLARFPLILDELLDPGSILVGPLAPSAYRDELGYTHAYLERDENDHOKRYTGGES
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                                                                                                                                       AlaLeuSerLysSerLeuAlaAspValAsnValLysCysAspPheValSerValProThr
                                                                                                                                                                       LeuAspArgTyrTrpTyrGlyProThrSerArgIleSerProGluAlaProValProVal
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     Length: Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                 (1-10641)
                                                 US-09-912-020-325 (1-477) x AE013955
     4.28e-118
2076.00
92.84%
86.11%
86.75%
                 Percent Similarity:
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Alignment Scores:
Pred. No.:
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AJ414144

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|GAAGAGTCA!GTTTCCTGGCTAATGCTGCCGGCGGTGTAGTGGGTGGGTAAATTGGGTACC
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                                                                                                                                                 GlyValMetThrGluGluGluLeuLysLeuAlaValAlaAlaAlaArgLysArgGlyGlu
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/poduct=10S ribosomal protein $21"
/poduct=10="0S ribosomal protein $21"
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RKRAKASAVKRHAKKLARENARRTRLY"
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                                                                                                                                                                                                                                               Parkhill, J., Wren, B.W., Thomson, N.R., Titball, R.W., Holden, M.T.G., Prantice, M.B., Sebaihia, M., James, K.D., Churcher, C., Mungail, K.L., Baker, S., Basham, D., Bentley, S.D., Brooks, K., Cerdeno-Tarraga, A.M., Chillingworth, T., Cronin, A., Davies, R.W., Davis, P., Dougan, G., Feltwell, T., Hamlin, N., Holroyd, S., Jagels, K., Leather, S., Karlyshev, A.V., Moulle, S., Oyston, P.C.F., Quall, M., Rutherford, K., Simmonds, M., Skelton, J., Stevens, K., Whitehead, S. and Barrell, B.G. Genome sequence of Yershia pestis, the causative agent of plague Nature, 413 (6855), 523-527 (2001)
                       BCT 06-JUN-2002
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                                                                                                                                                                           Versinia pestis
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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/gene="YP00645"
/note="Pfam match to entry PF01165 Ribosomal_S21,
Ribosomal protein S21, score 127.90, E-value 1.9e-34"
/gene="YP00645"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (04-0CT-2001) Submitted on behalf of the Yersinia
sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 ISA E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(92, .307)
/gene="YPO0645"
/note="Identical to Escherichia coli and Salmonella
Versinia pestis strain CO92 complète genome; segment 4/20.
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/db_xref="taxon:632"
/note="blovar: Orientalis"
complement(92, 307)
/gene="YPO0645"
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                                                                                            AJ41414.1 GI:15978734
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Parkhill, J.
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COMPLement(2149. .2214)
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/note="one of 5 probable transmembrane helices predicted
for YPO0647 by TMHMM2.0"
complement(2230. .2295)
/gene="XPO0647"
/gene="XPO0647"
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aldolase Folb SW.FOLB_ECOLI (P31055) (122 aa) fasta
scores: E(): 0, 84.7% id in 118 aa, and to Vibrio cholerae
putative dihydroneopterin aldolase VC0524 TR:09KUJ6
(EMBL.AE004138) (129 aa) fasta scores: E(): 2.9e-30, 67.2%
id in 116 aa"
                                                                                                                                                                                                                                                               /translation="MRVLGIETSCDETGIAVYDDKAGLLANQLYSQVKLHADYGGVVP
ELASRDHVRKTVPLIQAALKEANLSAKDÍDAVAYTAGPGLVGALLVGATIGRALAFAW
GVPAVPVHHMEGHLLAPMLEENAPEFPFVALLVSGGHTQLISVTGIGEYLLLGESVDD
                                                                                                                                                                                                                                                                                                                                                               AAGEAFDKTAKLIGIDYPGGPMLSRWAQQGTVGRFTFPRPMTDRPGIDFSFSGLKTFA
ANTIRANGDDDQTRADIARAFEDAVVDTLAIKSKRALDQTGFKRLVIAGGVSANQTLR
LKLADMMQKRGGEVFYARPEFCTDNGAMIAYAGWVRLRSNLNSELSVSVRPRWPLSEL
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//gene="YPO0647"
/note="Similar to Escherichia coli hypothetical protein
/rgih Sw.rGiH_ECOLI (P21056) (205 aa) fasta scores: E(): 0,
82.8 id in 204 aa, and to Haemophilus influenzae
hypothetical protein H10266 Sw.rGiH_HARIN (P44602) (199
aa) fasta scores: E(): 0, 67.3% id in 199 aa"
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(P05852) (337 aa) fasta scores: E(): 0, 87.8% id in 335
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complement(1972. .2622)
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/note="one of 5 probable t:
for YPO0647 by TMHMM2.0"
complement(2545. 2610)
/gene="YPO0647"
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for YPO0647 by TMHMM2.0"
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/gene="YPO0648"
/note="folb"
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and fasta scores: E(): 0, 91.3% id in 272 aa, and to
Bacillus subtlish yppothetical protein YubB TR:P94507
(EMBL:Z99119) (276 aa) fasta scores: E(): 0, 47.5% id in
                                                                                                                                                                                                                                                                                                                                                                                                                                                    predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3594. .3617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetLysValThrLeuProGluPheGluArgAlaGlyValMetValValGlyAspValMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                  rnote="one of 8 probable transmembrane helices for YPO0649 by TMHMM2.0"
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Conservative:
Mismatches:
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92.84%
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                    AAGCGGCTGAAAGGTGAAAAGCGGCCGGTTAATCCATTAGAACAACGTATGGTTGTCTTG 12409
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                                                                                                                                                                                                                                                                                                                                                                                                    GlnGlnMetIleGlnLeuAlaArgLysAlaGlyValProValLeuIleAspProLysGly 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AlaValValGlyLysCysLysThrGluGluGluIleValGluArgGlyMetLysLeuIle 220
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                                                                  AlaSerLeuGlyAlaAsnAlaArgLeuValGlyLeuThrGlyIleAspAspAlaAlaArg
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LLIEDSTADLALNNATFGSLTENNKTGKTSFIHHSLGTCNMSISSGYIYLAGNNDNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRQIVGKTLVQROKQVQEKENEVGSNSKRFLEEIATQAGFKVRVVNHYPHHCLRDCTY
PLYEQANHWRIFMYTPAVSSIRYATCLDDVVKNLTIFERNKELECLLKRYQYAHLEFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="hypothetical protein; identified by GeneMark;
putative"
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Sep 30, 1996 this sequence version replaced gi:1222265 Location/Qualifiers
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                                                       1. .14465

// Organism="Haemophilus influenzae

// Ob_ref="taxon:71421"

// 3. .579
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73. .579
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                              FEATURES
  COMMENT
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I (bases) to 14465)

Fleischmann, R.D., Adams, M.D., White, O., Clayton, R.A.,

Kirkness, E.F., Kerlavage, A.R., Bult, C.J., Tomb, J., Dougherty, B.A.,

Merrick, J.M., Morenney, K., Sutton, G.G., FitzHugh, W., Fields, C.A.,

Gocayne, J.D., Scott, J.D., Shirley, R., Liu, L.I., Glodek, A.,

Kelley, J.M., Weldman, J.F., Phillips, C.A., Spriggs, T., Hedblom, E.,

Cotton, M.D., Utterback, T., Hanna, M.C., Nguyen, D.T., Saudek, D.M.,

Geoghagen, N.S., Gnehm, C.L., McDonald, L.A., Small, K.V., Fraser, C.M.,

Smith, H.O. and Venter, J.C.

Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                              U32828 14465 bp DNA linear BCT 29-MAY-1998
Haemophilus influenzae Rd section 143 of 163 of the complete
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(Pases 1 to 14465)
White,O., Clayton,R.A., Kerlavage,A.R. and Fleischmann,R.D.
Direct Submission
Submitted (27-SEP-1997) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
The H. influenzae sequence has been updated by R. Fleischmann. New database matches have been assigned, product names have been improved, and a number of frame shifts have been corrected. We gratefully acknowledge the work of Tatusov et. al. We have incorporated their annotation into the /notes fields of the
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12410 GGTGCGTTGGAAGCGGTGGATTGGGTCGTGCCCTTTGAAGAAGATACGCCACAGCGTTTA 12469
                                                                                                                                                                                                                      Submitted (28-MAY-1998) The Institute for Genomic Research, 9712
                                                                                                                                   12470 ATTGCTGATATTTTGCCCGATCTGTTAGTCAAAGGCGGGGATTATAAGCCCCATGAAATT 12529
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Tatusov, R.L., Mushegian, A.R., Bork, P., Brown, N.P., Hayes, W.S.,
Borodovsky, M., Rudd, K.E. and Koonin, E.V.
Metabolism and evolution of Haemophilus influenzae deduced from
Whole-genome comparison with. Escherichia coli
Curr. Biol. 6 (3), 279-291 (1996)
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The whole genome was shifted by 588 nucleotides for a new start
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   White, O., Clayton, R.A., Kerlavage, A.R. and Fleischmann, R.D. Direct Submission
                                                                                421 IleAlaGlyIleLeuProAspLeuLeuValLysGlyGlyAspTyrLysProGluGluIle
                                                                                                                                                                                        441 AlaGlySerLysGluValTrpAlaAsnGlyGlyGluValLeuValLeuAsnPheGluAsp
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                                                                                                                                                                                                                                                                                                                                           GGCCGC 12634
                                                                                                                                                                                                                                                                                                 461 GlyCysSerThrThrAsnIleIleLysLysIleGlnGlnAspLys 475
                                                                                                            Db 12590 GGTGTCTCTACCACTATTATTCAGTCGATCAAA
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Haemophilus influenzae Rd
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032828.1 GI:1574362
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CDS	4118. 4270 /gene="H11524" /note="hypothetical protein; identified by GeneMark; putative"	Score: Percen Best L	Pred. No.: Score: Percent Similarity: Best Local Similarity:
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dene	Vicinistation in the Centribing SSSANIFCELNSASALDS VINCENITONS COMPLEMENT (4508 5245)	3 8	6844 GAATTTAAGCAAGC
CDS	/gene="H11545" /genplement(45085245)	δλ	27 GlyProThrSerAr
	/note="similar to GB:AE000666 percent identity: 32.51; identified by sequence similarity; putative"	qa	6784 GGCGCAACCAACCG
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gene	EAUQLE DERNSTOGS LEAR. CAODITEMENT (54326862)	qa	:: 6604 GAAAAACAAAAAT
CDS	/gene_ nijj20 /gene_ nij50 /gene_ nij56	Qy	107 LeuArgValLeuSe
	/gene- similar to PID:882153 percent identity: 97.38;	අු	6544 TTACGTATTTTATC
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	TITKLRILSRHQQLLRLDFEEDFŅNVDCKDLLAKLESAVKNYGALILSDYGKGTLKDV QKMIQIARKANVPVLIDPKGTDFERYRCATLLTPNMSEFEAVVGKCNTEEEIIEKGLK	δλ	167 AlaArgLysAlaGl
	LISDIELTALLVTRSEKGMTLLRPNQEPYHLPTVAKEVFDVTGAGDTVISVLATALAD GRSFEESCYLANVAAGIVVGKLGTSTVSTVELENAIHARPETGFGIMSEAELKDAVAQ	qq	6364 GCACGCAAAGCGAA
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	(htrb)" // / / / / / / / / / / / / / / / / /	οy	247 LeuHisMetProTh
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	FRAVPDICTTTGSYYLLKSSQNSKYIPFAPLRNKDGSGYTVSISAPVDFTDLQDETAI	<u>a</u>	6064 ATTAGCGTATTAGC
gene	DITIYMWLHR	δλ i	287 AlaAsnAlaAlaAla
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QKMIQLARQANIPVLIDPKGTDFERYRGATLLTPNMSEFEAVVGKCDSEEEITEKGLK
LIEQIDLSALLVTRSEKGMTLLRPNQPAFHLATEAKEVFDVTGAGDTVISVLATGLAD
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Pasteurella multocida PM70 section 94 of 204 of the complete
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St. Paul, MN
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GluLeuLysLeuAlaValAlaAlaArgLysArgGlyGluLysValValMetThrAsn
                                     5884 GAATTAAAAGATGCTGTCGCACAAAGCTAAAGCGCGGGGGAAAAATTGTGATGACTAAT
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                                                                                                                   347 GlyValPheAspIleLeuHisAlaGlyHisValSerTyrLeuAlaAsnAlaArgLysLeu
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Submitted (24-OCT-2000) Department of Veterinary
University of Minnesota, 1971 Commonwealth Ave.,
55108, USA
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	E. coli proliferat	E. coli cellular p	Escherichia coli p	. Salmonella typhi c	Pseudomonas aerugi	Neisseria meningit	H. pylori cytoplas	Protein encoded by	Pseudomonas aerugi	Enterococcus faeca
SUMMARIES		AAU34708	AAG98421	AAU38166	AAU36486	AAU72936	AAW20763	AAB07577	AAU36261	AAU35299
DB	21	22	22	22	22	23	18	21	22	22
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	26	154.5		ומינ	21	AAG09068	Arabidopsis thali
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	2 6	7 7	•	יי רי	27	ABB52865	ESCHETICHIA COLI
	35	148.5		n m	21	AAG09523	Arabidopsis thalia
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AC A	AAB1	15968;					
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×	편	coll prol	7	eration as	socı	associated protein s	sequence seg in NO:323.
KK	Escl	scherichia ntimicrobia	co]	i; E. col bacterial		<pre>i, proliferation; growth; antisense</pre>	inhibition; screening; e therapy; antibacterial.
S S	Esc)	scherichia	coli	;			
X A	WO2	00044906-	A2.				
X G	03-7	-AUG-2000.					
XX PF	27 -	JAN-2000:	200	000MO-US02200	200.		
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PR	27 -	JAN-1999;	6	9US-0117	405.		
A A	(ELIT	IT-) ELITRA		PHARM INC	. ;		
PI	Zys	Zyskind J, Yamamoto RT,	oh.Lse Xu	sen KL, u HH;	Trawick	ick J, Forsyth	th RA, Freelich JM, Carr GJ;
XX DR	WPI; N-PS	PI; 2000-5148 I-PSDB; AAA659	4822, 5973	2/46.			
X I	Novel	el polynucleotides	clec		od po	and polypeptides ass	ocia
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                                     AAA65809 to AAA65889 and AAA66058 to AAA66138 represent nuclectide sequences derived from Escherichia coli which inhibit E. coli proliferation. AAA65809 to AAA66055 and AAB15806 to AAB16040 represent nuclectide and protein sequences associated with E. coli proliferation. AAA66057 represent primers used for sequencing E. coli proliferation inhibiting nuclectide inserts in an example from the present invention. Methods from the present invention can be used to identify a proliferation-required gene in a microorganism, by contacting a microorganism with a proliferation-required gene activity inhibitory and inhibition occurs in the second microorganism, and determining if inhibition occurs in the second microorganism. The nucleic acid sequences identified as being required for bacterial growth and proliferation, can be used for antisense therapy for killing bacteria.
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 for use in antisense therapy
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                    Claim 11; Page 242-243; 316pp; English.
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used invention is also useful for the identification, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence tepresents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the will be the printed specification at the printed in the printed specification at the specification at the specification at the specific
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4.2e-208;
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100.0%; Pred. No. 4.2
:ive 0; Mismatches
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Xu HH;
                                                                                                                                                   ; 2000US-191078P.
; 2000US-206648P.
2000US-207727P.
; 2000US-242578P.
; 2000US-253625P.
; 2000US-253625P.
                                                                         21-MAR-2001; 2001WO-US09180
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23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
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27-SEP-2001
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(I) have antibacterial and antibiotic activities, and can be used in gene therapy. Expression of (1) in a microorganism inhibits proliferation of the microorganism, and the manufactured antibiotic is useful for reducing the activity or level of a gene product required for proliferation of a microorganism in a subject, specifically humans. The nucleic acids that inhibit bacterial growth or proliferation can be used as antisense therapeutics for killing bacteria. In addition to therapeutic applications, the nucleic acid sequences complementary to sequences required for proliferation can be used as diagnostic tools.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           For example, nucleic acid probes complementary to proliferation-required sequences that are specific for particular species of microorganisms can be used as probes to identify particular microorganism species in clinical specimens. AAH81295 to AAH81487 encode the Escherichia coli proteins given in AAG98239 to AAG98431, and AAH81488 to AAH81491 represent oligonucleotides, which are used in the exemplification of the
420
                                                                                               Novel nucleic acids encoding proteins required for Escherichia coli
proliferation, useful for screening for antimicrobial agents -
                                                                                                                                                                                      antimicrobial; antibacterial; antibiotic; gene therapy; diagnosis; bacterial growth inhibition.
                                                                                                                                                                IAGILPDLLVKGCDYKPEEIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQQDKKG 477
                                                                      ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL
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Pred. No. 4.2e-208;
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N-PSDB; AAH81477
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Length 477

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300
                                                         FEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKG 180
                                                                                                                                        TDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLL 240
                                                                                                                                                                                      QPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGT 300
                                                                                                                                                                                                                                    STVSPIELENAVRGRADTGFGVMTEEELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL 360
                                                                                                                                                                                                                                                                                  ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL 420
                                             ASEGANARI,VGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQOLIRLD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carr GJ;
 9
                                                                                                                                                                                                                                                                                                                              IAGILPDLLVKGGDYKPEEIAGSKEVWANGGEVLVLNFEDGCSTTNI1KKIQQDKKG 477
New polynucleotides for the identification and development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proliferation protein; design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella typhi cellular proliferation protein #57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wall
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                                                                                                                                                                                                                                                                                                                                                                                                              Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense; prokaryotic cellular antibiotic; antibacterial; drug
                                                                                                                                                                                                                                                                                                                                                                                                             AAU38166 standard; Protein; 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MXY-2000; 2000US-206848P.
26-MAY-2000; 2000US-207737P.
23-CCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-253655P.
22-DEC-2000; 2000US-257931P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-611495/70.
N-PSDB; AAS56025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella typhi
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Yamamoto RT,
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  δ
                                                                                             The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the discovery of novel antibiotics, the essential genes themselves and the discovery of novel antibiotics, the essential genes themselves and the discovery of novel antibiotic and the produces again and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein.

Sesential prokaryotic cellular proliferation protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ASLGANARLYGLTGIDDAARALSKTLAEVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 IDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 OPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 IAGILPDLLVKGGDYKPEEIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQQDKK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the printed specification, but was obtained in electronic rmat directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa cellular proliferation protein #476.
antibiotics, comprise sequences of antisense nucleic acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.7%; Score 2265; DB 22; 93.5%; Pred. No. 1.7e-196; ive 19; Mismatches 12;
                                                Example 3; Seq ID No 13759; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         477 AA;
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Matches
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential companies themselves and the encoded proteins. The prokaryotes used are scherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella compenionate, Pseudomonas aeruginosa and Enterococcus facealis. The promunoiae, Pseudomonas aeruginosa and Enterococcus facealis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to invention aused in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery comportances. The antisense nucleic acid sequence is also useful to screen for programmes. The antisense nucleic acid sequence is also useful to screen compounds in rational drug discovery compounds nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Contemporation in the sequence data for this patent did not form part of the printed specification, but was obtained in electronic
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proliferation protein; design.
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57.9%; Pred. No. 1.3e-113;
iive 70; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohlsen KL, Zyskind JW, Wall D,
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Antisense; prokaryotic cellular antibiotic; antibacterial; drug
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2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
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Matches 274; Conservative
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                                                                                                   Pseudomonas aeruginosa
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27-NOV-2000;
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The invention relates to a peptide (I) encoded by an operon (II) of Neisseria meningitidis including virulence genes, or a related molecule having a 40% sequence similarity at the peptide or nucleotide level in a Gram-negative bacterium, or its functional fragment, for therapeutic or diagnostic use. (I) and (II) are useful in the manufacture of a associated with infection by Neisseria condition (e.g., meningitis) associated with infection by Neisseria or Gram-negative bacteria. The product is useful for veterinary treatment and in a screening assay for the identification of an antimicrobial drug. The vaccines have prophylactic applications. AMU72911-AAU73014 represent N. meningitidis virulence proteins of the invention.
                                                                                                                                                                  419
                 360
                                                                                    300
                                                                                                                                 361 ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptide encoded by operon including virulence genes of Neisseria meningitidis, useful as vaccine component for treating or preventing meningitis and for identifying antimicrobial drug
241 QPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGT
                                                                                                                                                    301 STVSPIELENAVRGRADTGFGVMTEEELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meningitis; virulence; gene; antibacterial; vaccine; veterinary; Infection; Gram-negative bacteria; antimicrobial.
                                                                                                                                                                                                                     : : ||:||||||| |::||:|| |::|| | ||| || : ||| ||:|||:|| LEQVRPDVLVKGGDYGVEQVVGAQIVKAYGGEVRVLGLVENSSTTAIVEKIRQ 472
                                                                                                                                                                                                  IAGILPDLLVKGGDYKPEEIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQQ 473
                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis virulence protein #26.
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                                                                                                                                                                                                                                                                                                                   AAU72936 standard; Protein; 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAY-2001; 2001WO-GB02003.
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                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-066593/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAS97221
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                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                       AAU72936;
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The present sequence is a Helicobacter pylori cytoplasmic protein. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for OKF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various OKF were analysed for significant homology to other known or exported membrane proteins. Having identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
                              74 GLLSVTGNDEAADALDALMVQDGVASYLMRDKQIATTVKLRVVARNQQLIRLDFEEHPNR 133
                                                                                307
                                                              VDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKGTDFERYR 187
                                                                                                                            GATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLLQPGKAPL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                                                                                                                                                                                                               HMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGTSTVSPIE
RLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFEEGFEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H. pylori cytoplasmic protein, 07ap11409orf4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 61; Page 1174-1175; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mellgaerd
                                                                                                                                                                                                                                                                                                                                                                          AAW20763 standard; protein; 424 AA
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95US-0487032.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-052306/05.
                                                                                                                                                                                                                                                         LENAVRGRA 316
                                                                                                                                                                                                                                                                               113 LTKALSGOS 321
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                                                                                                                                                                                                                                                                                                                                                                                                         AAW20763;
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Length 323; Indels

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31.2%; Score 745.5; DB 23; 50.5%; Pred. No. 5.1e-59; ive 49; Mismatches 103;

156; Conservative

Similarity

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Matches

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Query Match

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(REGC ) UNIV CALIFORNIA
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RRI 486
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and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161
                                                                                                                                                                                                                                                                                                                                                                                                                            51 GGAANVAMNIASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSV-PTHPTITKLRV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              281 EEACFFANAAAGVVVGKLGTSTVSPIELENAVRGRADTGFGVMTEEELKLAVAAARKRGE 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341 KVVMTNGVFDILHAGHVSYLANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVL 400
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLM gene cluster; bleomycin gene cluster; polyketide metabolite;
bleomycin; bleomycin analogue; holo-carrier protein; thiazolidine;
thiazoline; bithiazoline; microbial metabolite; sugar.
                                                                                                                                                                                                                                                             3 GGAANVANNLISLKAKVFLCGVVGDDLKGKHFISTLNSIRIDTSGVLIDKTRCTTLKTRI
                                                                                                                                                                                                                                                                                                                                        63 IAQQQUVRVDKEI----KDPLNADLRKNLLDFIAEKIQEIDGVILSDYNKGVLDFELTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 LSRNQQLIRLDFEEGFEGVDP----QPLHERINQALSSIGALVLSDYAKGAL--ASVQ
                                                                                                                                                                                                                                                                                                                                                                                                   162 OMIQLARKAGVPVLIDPKGTDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D-YELSALLVTRSEQCMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25;
                                                                                                                                    Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein encoded by the bleomycin (BLM) gene cluster ORF30.
                                                                                                                               30.7%; Score 734.5; DB 18; Length 40.9%; Pred. No. 7.6e-58; ive 77; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB07577 standard; Protein; 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JAN-1999; 99US-0115435.
05-FEB-1999; 99US-0118848.
05-JAN-2000; 2000US-0477962.
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                                                                                                                             Query Match 30.79
Best Local Similarity 40.95
Matches 177; Conservative
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408 GYSTSAIIEKIKR 420
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                                                                                        424 AA;
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                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 LPVATDTGSRLLERAAGLLPAVDAVIVSDYGYG-VWEPDTVARLAAHRELGPSTLVVDSR 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 TGIDDAARALSKSL--ADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFEEGFEGVDP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 QP-----LHERINQALSSIGALVLSDYAKGALASVQQMIQLA--RKAGVPVLI--DP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 LDADGSLLFERDRPPVRTFARGSRAPVTAAVGAGDAFTAALTLALAAGADSAVAAELASA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FDILHAGHVSYLANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLECRMIVLGALEAVDW 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 VMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANARLVGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. VLVIGDVILDTYVWGATSGLCRESPVPAVTLTSVAHQCGGAANVAVNLRALGAEPVLLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 RPARFTALR-ASAVKPNHAEALRLLDAGEPPPGPARA-DWAAALGDRLLRLTGAERVALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 KGTDFERYRGATLLTPNLSEF-----EAVVGKCKTEEEIVERGMKLIADYELSALLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSEQGMSLLQPGKAPLHMPTQAQE--VYDVTGAGDTVIGVLAATLAAGNSLEEACFFANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGVVVGKLGTSTVSPIELENAVRGRADTGFGVMTEE-ELKLAVAAARKRGEKVVMTNGV
                                                                                                                                                                             nts useful for peptide and/or bleomycin, production and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.5%; Score 610.5; DB 21; Length 498; 37.7%; Pred. No. 1.7e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                 New bleomycin gene cluster components useful fcr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68; Mismatches 196;
Ε,
   Edwards
                                                                                                                                                                                                                          polyketide metabolites, especially bleomyc
chemically modifying biological molecules
                                                                                                                                                                                                                                                                                                                                Disclosure; Page 97-137; 162pp; English.
Chen M,
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Best Local Similarity 37.7
Matches 182; Conservative
   Sanchez
                                                                       2000-465974/40.
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                                                                                                         N-PSDB; AAA58471.
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the assential genes themselves and the discovery of novel antibiotics, the assential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneunoiae, Pseudomonas aeruginosa and Enterococcus faccalis. The invention is also useful for the antisense nucleic acids can also be used for antibiotic development. The antisense nucleic acids can also be used to antibiotic an be used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to ocreen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an expressent and a wide variety of crealular proliferation protein.
                                                                                                                                                  234 EQGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGV 293
                                                                                                                                                                             113 GGNGHLSPAVLARHEHLLEQ-----AQVVVCQLESPLETVGHVLRRAHALGKTVILNPAP 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carr GJ;
                                                                                             --KGTDFERFRGATLLTPNLSEFEAVVGKCKTEEEIVE---RGMKLIADYELSALLVTRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides for the identification and development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterococcus faecalis cellular proliferation protein #586.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chlsen KL, Zyskind JW, Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Seq ID No 10892; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 AA.
                                                                                                                                                                                                                                        294 VVGKLGTSTVSPI -- ELENAVRGRA 316
                                                                                                                                                                                                                                                                 AAU35299 standard; Protein; 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001US-269308P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-611495/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAS53158
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26-MAY-2000;
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27-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU35299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 EGFEGVDPQPL--HERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDP-- 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 QAKVLVVGSLAMDLVVRAPRLPRGGETLAGQSFITV------PGGKGANQAVAAARL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 RAGVMVVGDVMLDRYWYGPT----SRISPEAPVPVVKVNTIEERPGG-AANVAMNIASL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trawick JD,
                                                                                  Pseudomonas aeruginosa cellular proliferation protein #251.
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26.5%; Pred. No. 2.5e-09;
tive 50; Mismatches 153; Indels
                                                                                                                        Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Seq ID No 11854; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-253625P.
2000US-257931P.
2001US-269308P.
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2000US-207727P.
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                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohlsen KL,
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86; Conservative
                                                                                                                                                                                               Seudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-611495/70.
N-PSDB; AAS54120.
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                                                                                                                                                                                                                                    WO200170955-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                 23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
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Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2000;
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AAU36261;
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31-MAY-2002
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                                                                                    Sequence
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                                                                                                                                                                                                                                                             ----KGTDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSE 234
                                                                                    Gaps
                                                                                                   13 VMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGG---AANVAMNIASLGANARL 69
                                                                                                                                                  : |: | : | : | : | : | 110 MIYAGANNAFTPKQVQE--HQEIIEKSDFVIAQF-ESAIDSTIAAFKIAKKAGVKTILNP
                                                                                                                    VTIIGSINLD-----TTLRVK-EMPKPGETIHAIEHFTAGGGKGANQAVAAKRSGAETYF
                                                                                                                                        VGLTGIDDAARALSKSLA--DVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLD-----
                                                                                                                                                                           --FEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDP
                                                                                                                                                                                                                          QGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAG-NSLEEACFFANAAAGV
                                                                                   39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleotide sequences isolated from Pyrococcus abyssi encode proteins useful in industry -
                                                                 Length 305;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lecompte
                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Hyperthermophilic archaeon; hyperthermophilic protein.
                                                  Score 191.5; DB 22,
                                                               DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prieur D, Dietrich J, J, Saurin W, Heilig 1
                                                                        Best Local Similarity 22.8%; Pred. No. 7.8e
Matches 72; Conservative 63; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          Putative P. abyssi cytidylyltransferase #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Pages 1278-1279; 1657pp; French.
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(IFRE-) IFREMER INST FR RECH EXPL MER.
                                                                                                                                                                                                                                                                                                                                                      AAB96553 standard; Protein; 148 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99FR-0005034
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Weissenbach
                                                                                                                                                                                                                                                                                       294 VVGKLGTSTVSPIELE 309
                                                                                                                                                                                                                                                                                                        286 TVQRFGAQPSIPYQHE 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-126236/14.
                                              305 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pyrococcus abyssi
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Querellou J,
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                                               Sequence
                                                                 Query Match
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nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value sequences are selected of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.
a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up tl10 degrees centigrade.

Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AAH75903-AA
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39.9%; Pred. No. 4e-09;
iive 21; Mismatches 53;
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nes 55; Conservi
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                                                             119 MYPTYFVGRLGEDAHGKLIAEALGDDGCGVHLDYVRSVNNEPTGHAVVMLQSDGQNSIII 178
                                                                                                                      118 RLDFEEGFEGVD----PQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVP 173
                                                                                                                                                                                           230 VTRSEQGMSLLQPGKAPLHMP-TQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFAN 288
                                                                                    GANARLVGLTGIDDAARALSKSLAD -- VNVKCDFV -SVPTHPT -- - ITKLRVLSRNQQLI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carr GJ;
                                   Gaps
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                                                                                                                                                                    --GGAANVAMNIASL
                                                                                                                                                        174 VLIDPKGTDF----ERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALL
                                   49;
                  Length 379;
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                                                                                                                                                                                                                                                                                                                                              Haemophilus influenzae cellular proliferation protein #83.
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                 DB 23;
                7.6%; Score 181.5; DB 23; 25.6%; Pred. No. 8.6e-08; tive 45; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zyskind JW, Wall D,
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                                                  28 PTSRISPEAPVPVVKVNT-----IEERP-
                                                                                                                                                                                                                                                                                           AAU35442 standard; Protein; 306 AA.
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26-MAY-2000; 2000US-207727P.
23-CCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-253625P.
22-DEC-2000; 2000US-257931P.
16-PEB-2001; 2001US-269308P.
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                                  Conservative
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N-PSDB; AAS53301.
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379
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Sequence
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella preumoniae, Pseudomonas aeruginosa and Enterocccus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences.
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The invention relates to antisense inhibitors of genes essential to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                            Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                          E. coli cellular proliferation protein #394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Seg ID No 10406; 511pp; English.
                AAU34813 standard; Protein; 309 AA.
                                                                                                                                                                                                                                                                                                                           21-MAR-2001; 2001WO-US09180
                                                                                      14-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-611495/70.
N-PSDB; AAS52672.
                                                                                                                                                                                                                 Escherichia coli.
                                                                                                                                                                                                                                                     WO200170955-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haselbeck R,
                                                                                                                                                                                                                                                                                                                                                                                                                                  27-NOV-2000;
22-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                   23-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               famamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                 23-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-2000
                                                                                                                                                                                                                                                                                         27-SEP-2001
                                                  AAU34813;
 AAU34813
                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                                                        Sequences ABNY5021 trappesent 4534 nover number processor designated ORF (open reading frame) 1-4534 nover number of the ORF Company of the ORF Company of the ORF ORF ORF Company of the ORF ORF ORF Company of the ORF Nucleic acid sequences, vectors and host cells comprising ORF Company of the ORF nucleic acid sequences, vectors and host cells comprising ORF Company of the ORF nucleotides, the recombinant production of ORF proteins, antibodies of polynocleotides, methods of screening for modulators of ORFX expression or company of the ORFX proteins, antibodies specific for ORFX proteins, methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide company of biological activities, such as oytokine, cell proliferation, of the invention have a wide range of biological activities, such as oytokine, cell proliferation, framume modulation, haematopoisals requiration, classic acids and antihifammamentary activity, thrombolytic activity, chemotactic/chemokinetic acids and antihifammamentary activity, thrombolytic activity, chemotactic/chemokinetic acids and antihidalemnestry activity, thrombolytic activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. ORFX proteins, cother proliferative disorders such as peoused in the treatment of cancers, cother proliferative disorders such as sporiasis and benign tumours, cother proliferative disorders such as sporiasis and benign tumours, cother proliferative disorders such as sporiasis and benign tumours, corgan transplantation, disorders of tissue growth and regeneration, disorders in the detection of ORRY genomic sequences such as diabetes mallitus, hypothyroidism, and cholesterial cacids and probes, in the detection of ORRY genomic sequences in manners of the detection of ORRY genomic sequences in the detection of ORRY genomic sequences in the detection of ORRY genomic sequences in the detection of ORRY genomic sequences and probes, in the detection of OR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequences, in genetic diagnosis, and in forensic biology. The ORFX nucleic acids may additionally be used to produce transgenic animals which may be useful for studying the function and/or activity of ORFX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein, and in drug screening. The ORFX proteins may also be used as immunogens to generate specific antibodies, which are useful in the diagnosis, treatment and monitoring of ORFX-associated diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   378 ASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRLIAGILPDLLVKGGDYKP 437
                                                                                                                                                                                                                                                                    Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequences ABP31028-ABP35561 represent 4534 novel human proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.1%; Score 170; DB 23;
10.5%; Pred. No. 9.6e-08;
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                                                                                                                                                                                                                                                                                                                                                           Claim 10; Page 1338; 2508pp; English.
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                                                                   24-MAY-2001; 2001WO-US17076
                                                                                                   24-MAY-2000; 2000US-206690P
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                                                                                                                                                                             Shimkets RA;
                                                                                                                                           CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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N-PSDB; ABN77217.
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                                                                                                                                                                                                                                                                                                                           ransplantation
WO200190366-A2.
                                   29-NOV-2001
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Carr GJ;

Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Xu HH;

2000US-242578P. 2000US-253625P. 2000US-257931P.

2001US-269308P

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programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.
prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used and to obtain antibodies capable of binding to the expressed proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 ARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLKVLSRNQQLIRLDFEEGFE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 ERAGVMVV-GDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGG-AANVAMNIASLGAN 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 QNAGSLVVLGSINADHI----LNLQSFPTPGETVTGNHYQVAFGGKGANQAVAAGRSGAN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the printed specification, but was obtained in electronic format directly from WIPO at ttp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22; Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47; Mismatches 154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.1%; Score 169;
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Best Local Similarity 24.5%
Matches 77; Conservative
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58 IAFIACTGDDSIGESVRQQLATDNI 127 GVDPQPLHERINQALSSIGA
: :
175 LIDPKGTDFERYRGATLLTPNLSBFEAVVGKCKTEBEIVERGMKLIADYBLSALLVT 231 :::::::::::::::::::::::::::::::::::
164 ALNPAPARELPDELLALVDIITPNETEAEKLTGIRVENDEDAAKAAQVLHEKGIRTVLIT 223
232 RSEQGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAA 291
LGSRGVWASVNGEGQ-RVPGFRVQAVDTIAAGDTFNGALITALLEEKPLPEAIRFAHAAA 282
292 GVVVGKLGTSTVSP 305
283 AIAVTRKGAQPSVP 296

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2393
1 MKVTLPEFERAGVMVVGDVM......FEDGCSTINIIKKIQQDKKG 477
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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                                                                            sw model
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Gapop 10.0 , Gapext 0.5
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Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

PIR_73:* Database

pirl:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES

ADP-heptose syntha probable Kinase 24 ADP-heptose syntha ADP-heptose syntha ADP-heptose syntha ADP-heptose syntha LPS biosynthesis probable ADP-heptos probable adp-d-gly kinase [imported] ADP-heptose syntha ADP-heptose syntha probable DP-heptose probable DP-heptose probable bifunctio ribokinase - Therm probable sugar kin probable glycerol-ADP-heptose syntha glycerol-3-phospha aut protein NMB207 probable transfera aut protein - Alca fructokinase BH185 ribokinase (import ribokinase (EC 2.7 ribokinase (import ribokinase PA1950 Description B65093 G91120 F85965 AG0891 AI0080 C64127 A83022 F87700 H81319 C71887 G84936 0317 0320 B64627 H81154 H81951 139548 T34841 B å Query Match Length D 100.0 99.7 99.7 1712 1350.5 96.3 86.3 819.5 819.5 745.3 74 2393 2385 2385 2265 2076 188 184.5 184.5 183.5 Score Result Š

probable carbohydz

hypothetical prote	carbohydrate kinas	glycerol-3-phospha	ribokinase (EC 2.7	ribokinase rbsK [1	carbohydrate kinas	hypothetical prote	ructokinase [impo	probable kinase yi	probable kinase [1	ribokinase (EC 2.7	probable carbohydr	ribokinase - Deino	ribokinase (EC 2.7	ribokinase [import
H71120 F86307	D75288	A69427	B64073	Н84115	E75385	F84401	A96952 ·	E86076	F91229	T44955	D75260	A75599	KIECRB	F91215
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148 378	383	137	306	294	311	303	316	300	300	305	343	300	309	309
9.7	7.5	7.5	7.4	7.4	7.3	7.3	7.3	7.3	7.3	7.1	7.1	7.1	7.1	7.1
181.5	179.5	179	178	176	175	174	174	173.5	173.5	170.5	170.5	170	169	169
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1 B65093	
	ADP-hepto: N;Alternal	ADP-heptose synthase homolog - Escherichia coli (strain K-12) N'Alternate names: hypothetical protein b3052 C'Snecies: Escherichia coli
	C; Date: 1	C.Date: 10Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002 C.Date: 10. B45003
	R;Blattne.	RiBlattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y.
	A; Title: A; Referent	octence z//, 123-1402, 137, 137, 137, 138, 137, 137, 137, 137, 137, 137, 137, 137
	A; Accessic A; Status: A; Molecule	A;Accession: B65093 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
	A, Residue. A, Cross-r. A, Experime C, Superfar	A; Residues: 1-477 <blat> A; Cross-references: GBs.AE000387; GB:U00096; NID:g1789431; PIDN:AAC76088.1; PID:g17894 A; Experimental source: strain K-12, substrain M01655 C; Superfamily: hyporhetical protein b3052</blat>
	Query Match Best Local Matches 47	Query Match Best Local Similarity 100.0%; Pred. No. 1.1e-144; Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
		MKVTLPEFERAGVMVVGDVMLDRYWYGPTSRI SPEAFVPVVKVNTIEERPGGAANVAMNI
	Db 1	MKVTLPEFERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNI 60
	Qy 61	ASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLFVLSRNQQLIRLD 120
	Db 61	ASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLD 120
	Qy 121	FEEGFEGVDPQPLHERINQALSSIGALVLSDYARGALASVQQMIQLARRAGVPVLIDPKG 180
	Db 121	FEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKG 180
•	Qy 181	TDFERYRGATLLTPNLSEFEAVVGKCKTEBEIVERGMKLIADYELSALLVTRSEQGMSLL 240
	Db 181	TDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLL 240
	Qy 241	
	Db 241	QPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGT 300
	Qy 301	STVSPIELENAVRGRADTGFGVMTEEELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL 360
	Db 301	STVSPIELENAVRGRADTGFGVMTEEELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL 360
	Qy 361	ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL 420
	Db 361	

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ADP-heptose synthase (EC 2.7.-.) [imported] - Salmonella enterica subsp. enterica servar Typhi
C; Species: Salmonella enterica subsp. enterica servar Typhi
C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C; Accession: AG0891
C; Accession: AG0891
C; Accession: AG0891
C; Accession: AG0891
C; Authors: Parry, C; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Church
A; Authors: Parry, C; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se
A; Reference number: AB0502; PMID:11677608
A; Reference number: AB0502; PMID:11677608
A; Residues: 1-477 < CPAR>
A; Cross-references: GB:AL513382; PIDN:CAD07725.1; PID:g16504277; GSPDB:GN00176
C; Genetics:
A; Gene: rfaE
C; Superfamily: hypothetical protein b3052
C; Keywords: phosphotransferase
A;Reference number: A85480; MUID:21074935;.PMID:11206551
A;Accession: F85965
A;Status: preliminary
A;Notecule type: DNA
A;Residues: 1-477 < CSTO>
A;Cross-references: GB:AE005174; NID:g12517628; PIDN:AAG58186.1; GSPDB:GN00145; UWGP:A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z4405
C;Superfamily: hypothetical protein b3052.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLD
                                                                                                                                                                                                                                                                                                                                                                                        181 TDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 QPGKAPLHMPTQAQEVYDVTGAGDTVIGULATIATAAGNSLEEACFFANAAAGVVVGKLGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKVTLPEFERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNI
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                                                                                                                                                                                                                  Length 477;
                                                                                                                                                                                                              Score 2385; DB 2;
Pred. No. 3:6e-144;
1; Mismatches 1;
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                                                                                                                                                                                                                  Query Match 99.7%;
Best Local Similarity 99.6%;
Matches 475; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.78;
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                                                                                                                                      With the prose synthase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 05099 C; Species: Escherichia coli (c; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C; Accession: G91120 R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. By Reference number: A99629; MUID:21156231; PMID:11258796 A; Status: preliminary A; Molecule type: DNA A; Status: preliminary A; Molecule type: DNA A; Residues: 1-477 <HAXY A; Status: preliminary A; Wolecule type: DNA A; Residues: 1-477 <HAXY A; Status: Drawara A; Wolecule type: DNA A; Residues: 1-477 <HAXY A; Status: Drawara A; Wolecule type: DNA A; Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D.J.; Mayhev
K.; Apodaca,
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               IAGILPDLLVKGGDYKPEEIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQQDKKG 477
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Pred. No. 3.6e-144;
1; Mismatches 1;
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Best Local Similarity 99.6%;
Matches 475; Conservative
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C; Superfamily: }
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DPT-heptose synthase homolog - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Accession: C64127
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage; Gcoayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Wetdman, D.M.; Brandon, R.C.; Filter, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Science 269, 496-512, 1995
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: C64127
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Residues: 1-476 <TICR>
A, Cross-references: GB:U32828; GB:L42023; NID:g1574362; PIDN:AAC23172.1; PID:g1574367
C, Superfamily: hypothetical protein b3052
                                                                                                                                                                     STVSPIELENAVRGRADTGFGVMTEEELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL 360
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                                    241 QLGKPPLHLPTQAKEVFDVTGAGDTV1GVLAAALAAGNSLEESCFLANAAAGVVVGKLGT
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                                                                                    QPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGT
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C; Species: Yersinia pestis
C; Species: Versinia pestis
C; Species: Oz-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C; Accession: A10080
A; Farkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
Antitle: Genome sequence of Nersinia pestis, the causative agent of plague.
A; Reference number: AB0001; MUID:21470413; PMID:11586360
A; Recession: A10080
A; Accession: A10080
A; Residues: 1-476 <KUR>
A; Residues: 1-476 <KUR>
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                                                                 ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL
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                 Indels
 1.5e-136;
ches 12;
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86.1%; Pred. No. 1.6e-124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AL590842; PIDN:CAC89508.1;
C;Genetics:
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                 19; Mismatches
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C;Superfamily
C;Keywords: pl
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C, Accession: H81319
R; Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chill C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; Vanvliet, A.; Whitehead, S.; Bar Nature 403, 665-668, 2000
A; Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals A; Reference number: A81250; MUID:20150912; PMID:10688204
A; Accession: H81319
A; Accession: H81319
A; Status: Preliminary
A; Molecule type: DNA
A; Residues: 1-461 cPAR>
A; Residues: 1-461 cPAR>
A; Residues: 1-461 cPAR>
A; Cross-references: GB:AL139077; GB:AL11168; NID:96968444; PIDN:CAB73404.1; PID:9696
A; Experimental source: serotype O2, strain NCTC 11168
            Venter, J.C.; Fraser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable ADP-heptose synthase Cj1150c [imported] - Campylobacter jejuni (strain
                                                                                                                                                                                              A;Cross-references: GB:AE005673; NID:g13425394; PIDN:AAK25602.1; GSPDB:GN00148 C;Genetics: A;Gene: CC3640 C;Superfamily: hypothetical protein b3052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Campylobacter jejuni
C;Species: 31-Mar_2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 GANARLVGLTGIDDAARALSKSL-ADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFE 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPE-FERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASL
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                                                                                                                                                                                                                                                                                                                   Length 483;
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            Shapiro, L.;
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n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A.Title: Complete Genome Sequence of Caulobacter crescentus. A; Reference number: A87249; MUID:21173698; PMID:11259647
A; Accession: F87700
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-483 <STO>
                                                                                                                                                                                                                                                                                                                Query Match 37.8%; Score 904.5; DB 2; Best Local Similarity 45.1%; Pred. No. 5e-50; Matches 214; Conservative 66; Mismatches 186;
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Pred. No. 2e-47;
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C, Superfamily: hypothetical protein b3052
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C;Species: Caulobacter crescentus
C;Date: 2O-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: F87700
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-474 csTro.
A;Cross-references: GB:AE004912; GB:AE004091; NID:g9951274; PIDN:AAG08381.1; GSPDB:GN001
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                          P.; Hickey, M.J.; Br
A.; Larbig, K.; Lim,
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                                                                                                                                                                                                LPS biosynthesis protein RfaE PA4996 [imported] - Pseudomonas aeruginosa (strain PA01)
                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83022
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                                                                                                                                                                                                                      C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep_2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, a.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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                                                          DLLVKGGDYKPEEIAGSKEVWANGEVLVLNFEDGCSTTNIIKKIQ 472
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C;Superfamily: hypothetical protein b3052
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Matches 274; Conservative
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                               . 427
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C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C;Dates: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C;Accession: 684936
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp
A;Reference number: A84930; MUID:20445173; PMID:10993077
A;Accession: G84936
A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                AS---LEEIALILNQTHPKILPLEKL---LETLERNQQKIVFTNGCFDILHKGHASYLQK
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                                                                                                    TDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLL
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                                                                                GKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGTST
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                                     SKYSHASLITPNRAELEQALHLKLDSHANLSKALQILQETYHIAMPLVTLSEQGIAFLEK
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C;Species: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 811; DB 2; 1; Pred. No. 2.4e-44; 63; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              kinase [imported] - Buchnera sp. (strain APS)
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Matches 156; Conservative
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ETLNINELNSVL 312
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                                                                                243
                                                                                                                                                                                                 299
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B64627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable adp-d-glycero-d-mannoheptose synthase - Helicobacter pylori (strain J99)
C; Species: Helicobacter pylori
A; Varlety: strain J99
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Sep-1999
C; Accession: C71887
E; Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Isos, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A; Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A; Reference number: A71800; MUID:99120557; PMID:9923682
A; Status: preliminary
A; Molecule type: DNA
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-463 ARN>
A; Cross-references: GB:AE001509; GB:AE001439; NID:94155350; PIDN:AAD06368.1; PID:9415535
A; Experimental source: strain J99
C; Generics:
A; Gene: waa B
C; Superfamily: hypothetical protein b3052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 TGIDDAARALSKSLADVNVKCDFVSV-PTHPTITKLRVLSRNQQLIRLDFEEGFEGVDP- 130
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                                                                                                                                                                                                                       123 LENELIALFDEKIKDFKAVVLSDYAKGVLTPKVCKAVIEKAKVLNIPVLVDPKGSDFNKY 182
                                                                                                                                                                                                                                                                               RGATLLTPNLSEFEAVVGKCKTEEEIVERGM-KLIADYELSALLVTRSEQGMSLLQPGKA 245
                                                                                                                                                                                                                                                                                                                                                                                LGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRLIAGIL 425
                                                                                                                   LVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFEEGFEGV 128
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    Gaps
                                                         8 QKPKILIIGDFWVDNYTWCDCSRISPEAPVLIAKTLKEDKRLGGAANVYANLKSLGADVF 67
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                                         ERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANAR 68
                                                                                                                                                                                                                                                                                                                                                           246 PLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGTSTVSP
  20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.2%; Score 819.5; DB 2; Length 41.0%; Pred. No. 1.2e-44; Live 87; Mismatches 166; Indels
  90; Mismatches 158; Indels
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Matches 193; Conservative
  Conservative
203;
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Ouery Match
Best Local Similarity
Matches 159; Conserv
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Gene: rfaE; NMA1034
A; Gene: NMB0825
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A;Cross-references: GB:AE002435; GB:AE002098; NID:g7226049; PIDN:AAF41238.1; PID:g722606
A;Experimental source: serogroup B, strain MC58
C;Genetics:
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                     Ritchesion: B64627
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Ritchesion: S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne beterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A.Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A.; A. Seference number: A64520; MUID: 97394467; PMID: 9252185
A.; Reference number: A64520; MUID: 97394467; PMID: 9252185
A.; Reference number: A64520; Muid: Sequence not shown; translation not shown
                                                                                                                                                                                                                                                 A; Molecule, type: DNA—A; Residues: 1-461 <TOM>A; Residues: 1-461 <TOM>A; Residues: 1-461 <TOM>A; Residues: 1-461 <TOM>CIOSS-references: GB:AE000596; GB:AE000511; NID:g2313982; PIDN:AAD07904.1; PID:g231399 C; Superfamily: hypothetical protein b3052
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Datession: Hall54
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A. 14, Oin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandl, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
                                                                                                                                                                                                                                                                                                                                                                                                              6
  C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 VMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANARLVGL 72
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4 ILVIGDLIADYYLWGKSERLSPEAPVPVLEVQRESKNLGGAANVANNLISLKAKVFLCGV
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                                                                                                                                                                                                                                                                                                                                                              33.8%; Score 809.5; DB 1;
40.6%; Pred. No. 5.1e-44;
ative 88; Mismatches 165;
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A; Status: preliminary
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                                                                                                                                               8 FERAGYMYVGDYMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANA
                                                                                                                                                                                                                                                                                                                                                                                                                                              128 VDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKGTDFERYR
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s; Pred. No. 3.7e-40;
49; Mismatches 103;
                                                                             49; Mismatches 100;
   DB 2;
Score 753.5; . DB 2 Pred. No. 1.1e-40;
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Best Local Similarity 50.5%
Matches 156; Conservative
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C;Keywords: phosphotransferase
                                                                             Conservative
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probable bifunctional synthase /transferase - Streptomyces coelicolor C; Species: OS-Nov-1999 #text_change 21-Jan-2000 C; Accession: T34841
R; Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. Roliver, K.; Harris, Data Library, February 1999
A; Reference number: Z21559
A; Reference number: Z21559
A; Reference number: Z21559
A; Reference number: Z21559
A; Residues: Preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-463 < Coll>
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A; Collocule type: DNA
A; Residues: Laterences: EMBL:AL035478; PIDN:CAB36595.1; GSPDB:GN00070; SCOEDB:SC2G5.08
A; Cross-references: strain A3(2)
C; Genetics:
A; Gene: SCOEDB:SC2G5.08
C; Superfamily: hypothetical protein b3052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      356 HVSYLANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEED 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 PVPGTRLVTP--AEKEA-HGFAPSEGRPGGGLRAAALNAAALVRDWRVAAVTVTLGSRG-231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 24.8%; Score 594; DB 2; Length 463;
Best Local Similarity 36.3%; Pred. No. 2.6e-30;
Matches 173; Conservative 71; Mismatches 189; Indels 44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 VDPQPLHERINQALSSIG---ALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKGTDFE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 RYRGATLLTPNLSEFEAVVGKCKTE-----EEIVERGMKLIADYELSALLVTRSEQGM 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLLOPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGK 297
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

; Search time 38 Seconds November 24, 2002, 22:30:34 Run on:

(without alignments) 520.637 Million cell updates/sec

US-09-912-020-325 2393 1 MKVTLPEFERAGVMVVGDVM..........FEDGCSTINIIKKIQQDKKG 477 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ď			SUMMARIES		
Result		Query					
No.	Score	Match	Length	80	OI .	Desc	Description
П	2393	100.0	477	Н	RFAE_ECOLI	P7665	58 escherichia
63	1712		476	Н	RFAE_HAEIN	00200	74 haemophilus
М	819.5		463	Н	RFAE_HELPJ	Q9zkz0	
4	811	33.9	315	Н	Y060_BUCAI	P57168	.68 buchnera ap
S	809.5		461	Н	RFAE_HELPY	025529	
9	184.5	7.7	293	Н	RBSK_BACSU	P3694	_
7	178	7.4	306	Н	RBSK_HAEIN	P44331	
89	176	7.4	294	Н	RBSK_BACHD	Q9k6k1	_
σ	169	7.1	309		RBSK_ECOLI	P05054	54 escherichia
10	166.5	7.0	298	Н	YIHV_ECOLI	P3214	
11	164.5	6.9	320	Н	YDJE_BACSU	034768	
12	158	9.9	309	-	K6P2_ECOLI	P06999	
13	153	6.4	307	-	SCRK_VIBAL	P22824	24 vibrio algi
14	153	6.4	322	7	RBSK_HUMAN	Q9h477	
15	152.5	6.4	307	-	SCRK_SALTY	P26984	
16	151.5	6.3	148	-	YD36_METJA	058732	
17	150.5	6.3	318	-	RBSK_SCHPO	060116	
18	150	6.3	129	Н	TAGD_BACSU	P27623	23 bacillus su
19	145.5		307		SCRK_ECOLI	P40713	13 escherichia
20	142	5.9	307	Н	SCRK_KLEPN .	P26420	20 klebsiella
21	141	•	316	Н	K1PF_RHOCA	P2338	86 rhodobacter
22	135.5	٠.	544	-	CH60_NEIGO .	P298	٠.
23	133	5.6	370	-	CTPT_PLAFK	P49587	_
24	132.5		544	-	CH60_NEIMB	P423	
22	131		313	-	YEIC_ECOLI	P3023	35 escherichia
56	130.5		300	-	RBSK_LACLA	. 09cf4:	42 lactococcus
27	130.5		315		YDJH_ECOLI	. P7749.	93 escherichia
28	130.5		544	, 	CH60_NEIFL	P4821	
29	129.5	5.4	313	٦	K1PF_HAEIN	P44330	30 haemophilus
30	129.5	5.4	544	Н	CH60_NEIMA	P5700(
31	128	5.3	319	7	SCRK_SOLTU	P3782	<u> </u>
32	125.5	5.2	1182	Н	DP3A_RICPR .	00297	74 rickettsia
33	122.5	5.1	324	7	YM02_MYCTU	Q10391	91 mycobacteri

P33020 escherichia 033013 mycobacteri	Q49396 mycoplasma Q9qzc4 rattus norv	P25332 saccharomyc P23060 saccharomyc	Q99447 homo sapien P49583 caenorhabdi	Q64640 rattus norv P55263 homo sapien	Q9x5v3 rhizobium 1 O88022 streptomyce
YEII_ECOLI SR54_MYCLE	FRUK_MYCGE CTPU_RAT	RBSK_YEAST MK32_YEAST	PCY2_HUMAN CTPT_CAEEL	ADK_RAT ADK_HUMAN	ATCU_RHILV MMLC_STRCO
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362 521	369	333 363	389	361 362	841 705
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122.5 121	120.5	119.5 119.5	119.5	117.5	117 116.5
34 35	36	38 36	4 4 1	42 43	44

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                       180
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              61 ASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLD 120
                                                                                                                   240
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 ASLGANARLVGLTGIDDAARALSKSLADVNVKCDEVSVPTHPTITKLRVLSRNQQLIRLD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-RG / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M.
McKenlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Ulterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- PATHWAY: Lipopolysaccharide core biosynthesis.
                                                                                                                                                                                                                                                                                                                                               121 FEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKG
                                                                                                                   TDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLL
                                                                                                                                                                          QPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGT
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADP-heptose synthase (EC 2.7...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    476 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U32828; AAC23172.1; -. HSSP; P27623; 1COZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-99120557; And B.L., Brown E.D., Dolg P.C.,
Allm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Dolg P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria Nickelsen M., Mills D.M., Ives C.,
Grisson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
Tust T.J.;
                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                     16-0cT-2001 (Rel. 40, Created)
16-0cT-2001 (Rel. 40, Last sequence update)
15-0TN-2002 (Rel. 41, Last annotation update)
ADP-heptose synthase (EC 2.7.-.).
APP-heptose synthase (EC 2.7.-.).
Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                7 EFERAGYMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGAN
                                                                                                                                                                                                                                                                                                                                              67 ARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFEEGFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                247 LHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGTSTVSPI
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              Pfam; PF00294; pfkB; 1.
Pfam; PF01467; Cytidylyltransf; 1.
TIGRPAMS; TIGR01125; Cyt.tran.rel; 1.
PROSITE; PS00583; PFKB_KINASES_1; FALSE_NEG.
PROSITE; PS00584; PFKE_KINASES_2; FALSE_NEG.
Lipopolysaccharide biosynthesis; Transferase; Complete proteome.
SEQUENCE 476 AA; 51945 MW; 4F241C08D2C6951E CRC64;
                                                                                                                                                                                                                         ;
                                                                                                                                                                                   Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genomic sequence comparison of two unrelated isolates of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLLVKGGDYKPEEIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQ 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  427 DLLVKGGDYKPEEIAGSKEVWANGGDVKVLNFENGCSTINVIEKIK 472
                                                                                                                                                                               71.5%; Score 1712; DB 1; ilarity 71.0%; Pred. No. 5.2e-95; Conservative 58; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
IPR002173; PfkB.
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                                                                                                                                                                                                      Similarity
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Matches 331;
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STVSPIELENAV 312
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SEQUENCE FROM N.A.
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025529;
                                                                                                                                                                                                                                                                                           Query Match
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                     between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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            SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                  73 TGIDDAARALSKSLADVNVKCDFVSV-PTHPTITKLRVLSRNQQLIRLDFEEGFEGVDP- 130
                                                                                                                                                                                                                                                                                                                                                                183
                                                                                                                                                                                                                                                                                                                                                                                                              242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGTST 302
                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                  AS---LEEIALILNQTHPKILPLEKL---LETLERNQQKIVFTNGCFDILHKGHASYLQK
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                                                                                                                      InterPro; IPR004821; Cyt_tran_rel.
InterPro; IPR004820; Cytidylyltransf.
InterPro; IPR00243; PfkB.
InterPro; IPR00243; PfkB.
Pfam; PF00294; pfkB; I.
Pfam; PF00467; Cytidylyltransf; 1.
IIGRFAMS; TIGR00125; Cyt_tran_rel; 1.
PROSTTE; PS00584; PFKB_KINASES_1; FALSE_NEG.
PROSTTE; PS00584; PFKB_KINASES_1; FALSE_NEG.
Lipopolysaccharide blosynthesis; Transferase; Complete proteome. SEQUENCE 463 AA; 50926 MW; 770367403E771124 CRC64;
                                                                                                                                                                                                                                                        DB 1; Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GILPDLLVKGGDYKPEEIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQQ 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
NCBI_TaxID=118099;
                                                                                                                                                                                                                                                       34.2%; Score 819.5; DB 1;
41.0%; Pred. No. 6.5e-42;
Live 87; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical sugar kinase BUG60.
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                                                                                                     EMBL; AE001509; AAD06368.1; -.
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Matches 193; Conserv
                                                                                                                P27623; 1COZ
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P57168;
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MEDLINE-97394467; PubMed-9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Fletschmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                        Buchnera sp. APS.";
Nature 407:81-86(2000).
-i- SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter group;
                                                                                       H.;
aphids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKVTLPEFERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteome
                                                                                    , Sakaki Y., Ishikawa
bacterial symbiont of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Transferase; Kinase; Complete prv
SEQUENCE 315 AA; 35023 MW; 69B3707C601EFD25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93;
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Bacteria; Proteobacteria; epsilon subdivision;
Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.9%; Score 811; DB 1;
50.0%; Pred. No. 1.3e-41;
ive 63; Mismatches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADP-heptose synthase (EC 2.7...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002173; PfkB.
Pfan; PF00249; PfkB.1.
PROSITE: PS00543; PFKB_KINASES_1; 1.
PROSITE: PS00584; PFKB_KINASES_2; FALSE_NEG
SEQUENCE FROM N.A.
STRAIN-TOKYO 1998;
MEDLINE-20445173; Pubmed-10993077;
Shigenobu S., Watanabe H., Hattori M.,
"Genome sequence of the endocellular ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AP001118; BAB12783.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 VGDDLEGEHFISALKARGIDASGILIDKTRCTTLKTRIIAQNQQIARVDKEI----KDPL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----QPLHERINQALSSIGALVLSDYAKGAL--ASVQQMIQLARKAGVPVLIDPKGTDF 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 ARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRLIA 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANARLVGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M. Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                 -i- PATHWAY: Lipopolysaccharide core biosynthesis.
                                                                                         "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 ILVIGDLIADYYLWGKSERLSPEAPVPVLEVQRESKNLGGAANVANNLISLKAKVFLCGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 ERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIAD-YELSALLVTRSEQGMSLLQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKYSHASLITPNRTELEHALHLKLDSHANLSKALQILKETYHIAMPLVTLSEQGIAFLEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 GKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGTST
                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GILPDLLVKGGDYKPEEIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQQ 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : ||:||| || :|:||:|| alkpdilvkgadylnkevigse---Fakethlmefeegystsaiiekikr 457
                                                                                                                                                                                                                                                                                                                                                                                                                      Lipopolysaccharide biosynthesis; Transferase; Complete SEQUENCE 461 AA; 50688 MW; FB6A42A5301C16A5, CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .6e-41;
es_165;
                                                                                                                                                                                                                                                                                                                                                                             TIGREAMS; TIGRO0125; CYL_LTAD_rel; 1.
PROSITE; PS00583; PFKB_KINASES_1; FALSE_NEG.
PROSITE; PS00584; PFKB_KINASES_2; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.6%; Pred. No. 2.6e
tive 88; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.8%; Score 809.5;
                                                                                                                                                                                                                                                                                                             Interpro; IPR004821; Cyt_tran_rel.
InterPro; IPR004820; Cytidylyltransf.
InterPro; IPR002173; PfkB.
InterPro; IPR002173; PfkB.
Pfam; PF00294; pfkB; 1.
Pfam; PF01467; Cytidylyltransf; 1.
                                                                                                                                                                                                                                                                            EMBL; AE000596; AAD07904.1; -.
                                                                                                       pylori.";
Nature 388:539-547(1997).
-1- PATHWAY: Lipopolysacci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                        P27623; 1COZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
es 191; Conserv
                                                                                                                                                                                                                                                                                                    TIGR; HP0858
                                                                               Venter J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Guiseppi G., Guy B.J., Haja K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Guiseppi G., Guy B.J., Haja K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lepidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Taragi T., Takamaro H., Takamaru K.,
RA Vasarot V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Vastida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
R., The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Presecan E., Moszer I., Boursier L., Cruz Ramos H.C., De La Fuente V., Hullo M.-F., Lebrong C., Schleich S., Sekowska A., Scnq B.H., Villani G., Kunst F., Danchin A., Glaser P., The Bacillus subtilis genome from gerBC (311 degrees) to lick (334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- CATALYTIC ACTIVITY: ATP + D-ribose = ADP + D-ribose 5-phosphate.
-:- PATHWAY: Ribose metabolism; first step.
-:- SUBCELLULAR LOCATION: CYtoplasmic (By similarity).
-:- SIMILARITY: BELONGS TO THE PPKB FAMILY OF CARBOHYDRATE KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Analysis of a ribose transport operon from Bacillus subtilis.";
Microbiology 140:1829-1838(1994).
                                                                                                                                                                                                                                                                                                                                                            Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                 P36945; P96733;
01-JUN-1994 (Rel. 29, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
1-JUN-2002 (Rel. 41, Last annotation update)
Ribokinase (EC 2.7.1.15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98015417; PubMed=9353933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Microbiology 143:3313-3328(1997).
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Woodson K., Devine K.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 Bacillus subtilis,
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-1423;
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                                                                                                                                                                                                                                                                                                                                                                     Bacteria;
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Matches
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 entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                     118 -RLDFEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLI 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DP---KGTDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 LTGIDDAARALSKSLADVNVKCDFVSVPTH-PTITKLRVLSRNQQLI------- 117
                                                                                                                                                                                                                                                                                                                                                                            60 KVGDDHYGTAILNNLKANGVRTDYMEPVTHTESGTAHIVLAEGDNSIVVVKGANDDITPA 119
                                                                                                                                                                                                                                                                                                                                                                                                                             120 YALNALEQIEKVDMVLIQQEIPE-------ETVDEVCKYCHSHDIPIIL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-Rd / KW20 / ATCC 51907;
STRAIN-Rd / KW20 / ATCC 51907;
STRAIN-Rd / KW20 / ATCC 51907;
MEDLINE-9536030; Publed-7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKerney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                 13 VMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGG-AANVAMNIASLGANARLVG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGV
                                                                                                                                                                                                                                                                                                                         4 ICVIGSCSMDLV -- - VTSDKRPKAGETVLG -TSFQTVPGGKGANQAVAAARLGAQVFMVG
                                                                                                                                                                                                                                                                       51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                          Transferase; Kinase; Complete protecome.

CONFLICT 284 293 TRNEVEELLS -> DKK (IN REF. 1).

SEOUENCE 293 AA; 31138 MW; DCB69533E53253EE CRC64;
                                                                                                                                                                                                                                                          ; Pred. No. 0.00023; 41; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
115-JUN-2002 (Rel. 41, Last annotation update)
RBSK OR HI0505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA.
                                                                                                                                                                                                                                              7.7%; Score 184.5;
             or send an email to license@isb-sib.ch)
                                                                                                                                        Pfam, PF00294; pfkB; 1.
PRINTS; PR00990; RIBOXINASE.
PROSTIE: PS00583: PFKB_KINASES_1: 1.
PROSTIE: PS00584; PFKB_KINASES_2: 1.
                                                                                                               InterPro; IPR002173; PfkB.
InterPro; IPR002139; Ribokinase.
                                  EMBL; 225798; CAA81049.1; -.
EMBL; 292953; CAB07465.1; -.
EMBL; 299122; CAB15609.1; -.
PIR; S42711; S42711.
HSSP; P05054; IRKD.
Subtillist; BG10877; rbsK.
                                                                                                                                                                                                                                                          Local Similarity 25.3%;
nes 80; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 VVGKLGTSTVSPIELE 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    272 SVCSFGAQGGMPTRNE 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=727;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
"Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 GGAANVAMNIASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 SRNQQLIRLDFEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMI---- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199 FEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLLQPGKAPLJIMPTQAQEVYD 258
                                                                                                -:- CATALYTIC ACTIVITY: ATP + D-ribose = ADP + D-ribose 5-phosphate.
-:- PATHWAY: Ribose metabolism; first step.
-:- SUBCELLULAR LOCATION: CYCOPLASSMIC (By similarity).
-:- SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARROHYDRATE KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 AEILTGVEVADEQSAVKAASVFHDKGIETVMITLGAKGVFVSRKGKSRIIKGFCVQAI-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 GKGANQAVAAARLGAKVAFISCIGSDSIGKTMKNAFAQEGID-----TTH-----IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 VTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGTSTVSFIELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus NCBI_TaxID=86655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transferase; Kinase; Complete proteome.
SEQUENCE 306 AA; 32204 MW; 3DCE8810827C8E84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-C-125 / JCM 9153; MEDLINE-20512582; PubMed-11058132; Takami H., Nakasone K., Takaki Y., Maeno G., Sasakā R. Takahi F., Hirama C., Nakamura Y., Ogasawara N., Kuhara Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 0.00059; 45; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.4%; Score 178; DB 1; 22.7%; Pred. No. 0.00059;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pfam; PF00294; pfkB; 1.
PRNTS; PR00990; RIBOKINASE.
PROSITE; PS00583; PFKE_KIRASES_1;
PROSITE; PS00584; PFKE_KIRASES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002173; PfkB.
InterPro; IPR002139; Ribokinase.
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15-JUN-2002 (Rel. 41, Last seq
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U32732; AAC22163.1; -. HSSP; P05054; 1RKD.
                                                             Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ribokinase (EC 2.7.1.15).
RBSK OR BH3728.
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Q9K6K1;
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STRAIN=K12
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                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 VGLTGIDDAARALSKSLADVNVKCDFVSVPTHPT--ITKLRVLSRNQQLI------R 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 IGRVGDDPFGHVLTENLAKEGIITDSVKPVTDCTSGVATILLSDRDNRIIVTKGANEHVT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 LDFEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDP 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235 QCMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVV 294
          halodurans and genomic sequence comparison with Bacillus subtilis.";
Nucleic Acids Res. 28:4317-4331(200).
1-1 CATALYTIC ACTIVIY: AT-+ b-ribose = ADP + D-ribose 5-phosphate.
1-1 PATHWAY: Ribose metabolism; first step.
1-1 SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
1-1 SUBCELLULAR ELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.
                                                                                                                                                                                                                                                                                                                                                                            13 VMVVGDVMLDRYWYGPTSRISPEAPV--PVVKVNTIEERPGG-AANVAMNIASLGANARL 69
                                                                                                                                                                                                                                                                                                                                                                                                  6 ITVVGSINMDMV-----TITDVVPVQGETVLGKDFRTVPGGKGANQAVAAARLGANVRM 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 PDYVAAFE-----QELAASDVVLLQ--LEIPLETVAYVLEFCAKHHVTTVLNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
"Complete genome sequence of the alkaliphilic bacterium Bacillus
                                                                                                                                                                                           EMBL; Arvatar.;
HSSP; PG5054; 1RK2.
HSSP; PG5054; 1RK2.
InterPro; IPR002173; PfkB.
InterPro; JPR002199; Rbokinase.
R PRINTS; PR00390; RISDKINASE.
R PRNTS; PS00584; PFKB.KINASES.1; 1.
JR PROSITE; PS00584; PFKB.KINASES.2; 1.
JR PROSITE; PS00584; PFKB.KINASES.2; 1.
KW Transferase; Kinase; Complete proteome.
Transferase; Kinase; Complete proteome.
Transferase; Kinase; Complete proteome.
                                                                                                                                                                                                                                                                                                                          Length 294;
                                                                                                                                                                                                                                                                                                                                                  49; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                          7.4%; Score 176; DB 1; 25.4%; Pred. No. 0.00074;
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Ribokinase (EC 2.7.1.15).
RBSK OR B3752 OR Z5253 OR ECS4694.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            309 AA
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                                                                                                                                                                                                                                                                                                                                                  80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 VGKLGTSTVSPIELE 309
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SEQUENCE FROM N.A.
STRAIN=K12;
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P05054;
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MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE=90179935; PubMed=9519409; Sigrell J.A., Cameron A.D., Jones T.A., Mowbray S.L.: "Structure of Escherichia coli ribokinase in complex with ribose and dinucleotide determined to 1.8-A resolution: insights into a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        + D-ribose 5-phosphate.
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=K12 / MG1655.
MEDLINE=93315143; PubMed=7686882;
MEDLINE=93315143; PubMed-7686882;
MEDLINE=93315143; PubMedt G. III, Daniels D.L., Blattner F.R.;
"DNA sequence and analysis of 136 kilobases of the Escherichia coli genome: organizational symmetry around the origin of replication.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sigrell J.A., Cameron A.D., Jones T.A., Mowbray S.L.; "Purification, characterization, and crystallization of Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
MEDLINE=86224052; PubMed=3011794;
Hope J.N., Bell A.W., Hermodson M.A., Groarke J.M.;
Kibokinase from Escherichia coli K12. Nucleotide sequence and
overexpression of the rbsk gene and purification of ribokinase.";
J. Biol. Chem. 261:7663-7668(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=0157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glisner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Agrodbeck B.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS).
MEDLINE=99370056; PubMed=10438599;
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MEDLINE=98046763; PubMed=9385653;
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-!- SUBUNIT: HOMODIMER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      family of kinase structures."; Structure 6:183-193(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics 16:551-561(1993).
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15-DEC-1998 (Rel. 37, Created)
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034768;
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                                                                                                                                                                                                                                                                                                                                                                                         106 GENVIGIHAGANAALSPALVEAQRERIANASALLMQ--LESPLESVMAAAKIAHQNKTIV 163
                                                                                                                                                                                                                                                                                                                                                                                                                175 LIDP---KGTDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 RSEQGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAA 291
                                                                                                                                                                                                                                                                                                                                                                   127 GVDPQPLHERINQALS-----SIGALVLSDYAKGALASVQQMIQLARKAGVPV 174
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                           ERAGVMVV-GDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGG-AANVAMNIASLGAN 66
                                                                                                                                                                                                                                                                                                 2 QNAGSLVVLGSINADHI----LNLQSFPTPGETVTGNHYQVAFGGKGANQAVAAGRSGAN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93347969; PubMed=8346018; Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.; Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.; Fanalysis of the Escherichia coli genome. III. DNA sequence of the region from 87.2 to 89.2 minutes."; Nucleic Acids Res. 21:3391-3398(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                      36;
                                                                                                                                                                                                                               Length 309;
                                                                                                                                                                                                                            Query Match 7.1%; Score 169; DB 1; Length 305
Best Local Similarity 24.5%; Pred. No. 0.002;
Matches 77; Conservative 47; Mismatches 154; Indels
                                                                                                                                                        PRINTS; PRO090; RIBOKINASE.
PROSITE; PSO0583; PFKB_KINASES_1; 1.
PROSITE; PS00584; PFKB_KINASES_2; 1.
Transferase; Kinase; 3D-structuse; Complete proteome.
SEQUENCE 309 AA; 32290 MW; 75372984 ib64060E CRC64;
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15-DEC-1998 (Rel. 37, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical sugar kinase yihv.
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                                                                                      PDB; IRKA; 20-MAR-00.
PDB; IRKS; 31-AUG-99.
EcoGene; EG10818; rbsK.
InterPro; IPR002173; PfkB.
InterPro; IPR002193; Ribokinase.
Pfam; PF00294; pfkB; 1.
                    AE000452; AAC76775.1; -. AE005607; AAG58955.1; -. AP002566; BAB38117.1; -.
          L10328; AAA62105.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 GVVVGKLGTSTVSP 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 AIAVTRKGAQPSVP 296
                                                      PIR; A26305; KIECRB.
PDB; 1RKD; 04-MAR-98.
PDB; 1RK2; 07-JUN-00
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STRAIN-K12 / MG1655;
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P32143;
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EMBL;
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or send an email to license@isb-sib.ch).
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MEDLINE=98116660; PubMed=9455482;
Kasahara Y., Nakai S., Ogasawara N., Yata K., Sadaie Y.;
Kasahara Y. Of the GroESL-CotA region of the Bacillus subtilis genome, containing the restriction/modification system genes.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 -----ITPQDISELVALSDHAAFSEPGLARLTGVKEMASALKOAQTLTNGHVYVTQGSA 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 TGIDDAARAESKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFEE-----GFEG 127
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EMBL; AE000464; AAD13445.1; ALT_INIT.

PIR; $40827; $40827.

ECOGENE; EG11848; yihv.

PICAPPRO: IPR00213; PfkB.

PROSTIE; PS00534; PFKB_KINASES_1; FALSE_NEG.

PROSTIE; PS00534; PFKB_KINASES_2; 1.

PROSTIE; PS00634; PFKB_KINASES_2; 1.

PROSTIES PS00645; PFKB_KIN
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15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, La
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MEDLINE=98044033; PubMed=9384377;
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Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., An Eritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Gham S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guiseppi G., Glay B.J., Hadga K., Halcoh J., Harwood C.R., Henaut A., Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C., Median N., Mellando R.P., Mazuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Schrout E., Schleich S., Schroeter R., Scoffone F., Schich J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Arseuchi M., Tamakoshi A., Tanaka T., Takamata P., Togonon A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Vannanch B., Van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 LTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIR-LDFEEG----- 124
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SEQUENCE 320 AA; 34256 MW; A54E095039953B7A CRC64;
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InterPro; IPR002173; PfkB.
Pfam. PF00294; pfkB, 1.
PROSITE; PS00583; PFKB_KINASES_1; 1.
PROSITE; PS00584; PFKB_KINASES_2; 1.
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HSSP; Q9TVW2; 1DGY.
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Les 80; Conservative
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Nature 390:249-256(1997).
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               P06999; P78065; P78260; 01-APR-1988 (Rel. 07, Created) 01-NPR-1998 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 6-phosphofructokinase isozyme 2 (EC 2.7.1.11) (Phosphofructokinase) PFKB OR B1723.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular cloning of the gene for phosphofructokinase-2 of
Escherichia coli and the nature of a mutation, pfkBl, causing a high
level of the enzyme.";
J. Mol. Biol. 168:285-305(1983).
-!- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate " ADP + D-
fructose 1,6-bisphosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- MISCELLANEOUS: ONLY 10% OF THE ACTIVITY PRESENT IN THE WILD-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- ENZYME REGULATION: PFK-2 IS SENSITIVE TO INHIBITION BY FRUCTOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97426617; PubMed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shoo Y.; "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHOFRUCTOKINASE 2.

-!-SIMILARITY: PHOSPHOFRCTOKINASE-1 SHOWS NO HOWOLOGY TO
SIMILARITY: PHOSPHOFRCTOKINASE-2. THE MINNR PHOSPHOFRUCTOKINASE FOUND IN
E.COLI. ALTHOUGH THE REACTION CATALYSED IS THE SAME, THE TWO
ENZYMES HAVE A DIFFERENT EVOLUTIONARY ORIGIN.
-!- SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alba H., Baba T., Fullta K., Hayashi K., Inada T., Isono K., Itoh Kasai H., Rashimoto K., Kimura S., Kitakawa M., Kitagawa M., Mashimoto K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Gshima T., Saito Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Takedo J., Ashorb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN IS PHOSPHOFRUCTOKINASE-2.
-!- MISCELLANEOUS: THIS ENZYME IS NOT TO BE CONFUSED WITH
6-PHOSPHOFRUCTO-2-KINASE (EC 2.7.1.105), WHICH IS ALSO CALLED
                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                       minor
                                                                                                                                                                                                                                                                                                                              "Nucleotide sequence of gene pfkB encoding the phosphofructokinase of Escherichia coli K-12." Gene 28:337-342(1984).
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309 AA
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                                                                                                                                                                                                                                                                                         MEDLINE-84262485; PubMed-6235149;
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
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                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                               Escherichia coli.
                                                                                                                                                                                                         NCBI_TaxID=562;
                                                                                                                                                                                                                                                                          STRAIN=K12;
K6P2_ECOLI
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Wightman P.J
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Q9H477;
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         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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There are no restrictions on ig as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                             79 ARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFE---EGFEGVDP---- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----QPLHERINQALSSIGALVLSDYAKGA-LASVQQMIQLARKAGVPVLIDPKGTDFER 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 YRGA-----TLLTPNLSEFEAVVGK------CKTEEEIVERG--MKLIADYELSALL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 LSAALAIGNIELVKPNQKELSALVNRELTQPDDVRKAAQEIVNSGKAKRVVVSLGPQGAL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230 VTRSEQGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 GVDSENCIQVVPP------PVKSQ---STVGAGDSMVGAMTLKLAENASLEEMVRFGVA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                     -EHLVSLLADENV------PVATVEAKDWTRQNLHVHVEASGEQYRFVMPGAALN 114
                                                                                                                                                                                                                                                                                                                                                                                              TSRISPE-----APVPVVKVNTIEERPGGAANVAMNIASLGANARLV----GLTGIDDA 78
                                                                                                                                                                                                                        rransferase; Kinase; Glycolysis; Complete proteome.
confiler 26 38 GKLRCTAPVEBPG -> ENCAVPHRCSNP (IN REF. AND 4).
                                                                                                                                                                                                                                                           AAQKQĞIRCIVDSSGEA -> LRKNKGSAASSTVLGQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio alginolyticus.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=663;
                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                Length 309;
                                                                                                                                                                                                                                                                                                                               ; Score 158; DB 1; Length 309; Pred. No. 0.0092; 37; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                          A93BEBE0D5801309 CRC64;
                                                                                                                                                                                                                                                                       (IN REF. 1).
PV -> AL (IN REF. 1).
SM -> RL (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-NUV-1995 (Rel. 32, Last annotation update)
Fructokinase (EC 2.7.1.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 AA
                                                                                                                                                                                                                                                                                                                                 6.6%; Score 158;
25.4%; Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-91071601; PubMed-2174811;
Blatch G.L., Scholle R.R., Woods D.R.;
European Bioinformatics Institute.
                                                                              EMBL; AE000267; AAC74793.1;
EMBL; D90814; BAAL5500.1; ALT_INIT.
EMBL; D90815; BAAL5506.1; ALT_INIT.
EMBL; K00128; AAA24320.1; -
PIR; AA4950; KIECPB
SWISS-2DPAGE; P065999; COLI.
ECO2DBASE; E036.6; GTH EDITION.
                                                                                                                                                             Ecocene; EG10700; pfkB.
InterPro; IPR002173; PfkB.
Pfam, PF00294; pfkB. 1.
PROSITE; PS00583; PFKB.KINASES_1: 1.
PROSITE; PS00584; PFKB_KINASES_2: 1.
                                                                                                                                                                                                                                                                                  245 246 1 257 258 309 AA; 32456 MW;
                                                                     EMBL; K02500; AAA24321.1; -.
                                                                                                                                                                                                                                                                                                                                                        80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            282 AGSAATLNQGTRLCS 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 AAGVVVGKLGTSTVS 304
                                                                                                                                                                                                                                                            171
                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                            155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
SCRK_VIBAL
ID SCRK_VIBAL
AC P22824;
                                                                                                                                                                                                                                                                                 CONFLICT
CONFLICT
SEQUENCE
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Best Local S
Matches 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 QPLHERINQALS--SIGALVLSDYA-----KGALASVQQM1QLAKKAGVPVLIDPK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224 ELSALLVTRSEQGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNS---- 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequence and analysis of the Vibric alginolyticus sucrose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 LTGIDDAARALSKSLADVNVKCDF-VSVPTHPTITKLRVLSRNQQLIRLDFEEGFEGVDP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 FMVKPSADQFMSVEDMGNFKQGDWLHVCSISLANEPSRSSTFEAIKRAKAAGGFISFDPN 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 VMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGA-ANVAMNIASLGANARLVG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 VWVTGDAVVD------LIPESETSLEKC-----PGGAPANVAVAIARLSGKSAFFG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RVGDDPFGRFMQSILDQEGVCTEFLIKDPEQRTST------VVVDLDDQGERSFT 97
                                                                                                                                             phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTDFERYRGATLLTPNLSEFEAVVGKCK-----TEEEI-----VERGMKLIADY
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae: Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70;
                                                                                                         -!- CATALYTIC ACTIVITY: ATP + D-fructose = ADP + D-fructose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fransferase, Kinase.
SEQUENCE 307 AA; 33045 MW; AF9C96CBB781C6EF CR:64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.4%; Score 153; DB 1;
Best Local Similarity 23.5%; Pred. No. 0.018;
Matches 78; Conservative 53; Mismatches 131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ribokinase (EC 2.7.1.15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wightman P.J.;
Thesis (2000), University of Edinburgh, U.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 PVVSSAIQWANGCGALATTQKGAMTALPTQTE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfan, PF00294; pfkB; 1.
PROSITE; PS00583; PFKB_KINASES_1; 1.
PROSITE; PS00584; PFKB_KINASES_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M76768; AAA27556.1; -. PIR; JQ0782, LQ0782. HSSP. O9TWA2; LGGY. InterPro; IPR002173; PfkB.
                                    uptake-encoding region.";
Gene 95:17-23(1990).
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SEQUENCE FROM N.A.
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                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPT-----ITKLRVLSRNQQL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGAMTSMVCKVGKDSFGNDY1ENLKQNDISTEF----TYQTKDAATGTASIIVNNEGQNI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 IRLDFEEGFEGVDPQPLHERINQALSSIG-ALVLSDYAKGALASVQQMIQLARKAGVPVL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----IITLGAEGCVVLSQTEPEPKHIPTEKVKAVDTTGAGDSFVGALAFYLAYYPNLSL 287
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERP-----GGAANVAMNIAS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
--- CATALYTIC ACTIVITY: ATP + D-ribose = ADP + D-ribose 5-phosphate.
--- PATHWAY: Ribose metabolism; first step.
--- SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 IDP----KGTDFERYRGATLLTPNLSEFEAV----VGKCKTEEE----IVERGMKLIADY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 FNPAPAIADLDPQFYTLSDVFCCNESEAEILTGLTVGSAADAGEAALVLLKRGCQVV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224 ELSALLVTRSEQGMSLL-QPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLA--AGNSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                               54;
                                                                                                                                                                                                                                                                                                                                                                                                 Score 153; DB 1; Length 322; Pred. No. 0.019;
                                                                                                                                                                                                                                                                                                                                                                                                                            48; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                      322 AA; 34143 MW; 50D0E7161F33E94B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307 AA.
                                                                                                                                                                                                                                                                                                                           PROSITE; PS00583; PFKB_KINASES_1; FALSE_NEG PROSITE; PS00584; PFKB_KINASES_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      281 EEACFFANAAAGVVVGKLGTSTVSP 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDMLNRSNFIAAVSVQAAGTQSSYP 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
MEDLINE-92236409; PubMed=1809835;
                                                                                                                                                                                                                                                               InterPro; IPR002173; pfkB.
InterPro; IPR002139; Ribokinase.
Pfam: PF00294; pfkB; 1.
PRINTS; PR00990; RIBOKINASE.
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01-AUG-1992 (Rel. 23, Last segu
01-AUG-1992 (Rel. 23, Last anno
                                                                                                                                                                                                                     EMBL; AJ404857; CAC12877.1; -. EMBL; BC017425; AAH17425.1; -. HSSP; P05054; 1RK2.
                                                                                                                                                                                                                                                                                                                                                                                                  6.4%;
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Best Local Similarity 25.5%
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                                                                                                                                                                                                                                                                                                                                                         Transferase; Kinase.
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NCBI_TaxID=602;
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P26984;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 QLIRLDFEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 AKVWVLGDAVVD-----LLPESE-----GRLLQCPGGAPANVAVGVARLGGNSGF 47
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                                                                                                                                                                                                                                                                                                                                                                                  phosphate.
SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.
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                                                                                                                                                                                                                                                  MOl. Microbiol. 5:2913-2922(1991).
-!- CATALYTIC ACTIVITY: ATP + D-fructose = ADP + D-fructose 6-
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Aulkemeyer P., Ebner R., Heilenmann G., Jahreis K., Schmid K. Wrieden S., Lengeler J.W.; Wolecular analysis of two fructokinases involved in sucrose metabolism of enteric bacteria.
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37 AA; 32916 MW; E01CB770CE20B329 CRC64:
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13.8%; Pred. No. 0.019;
ve 48; Mismatches 126;
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PIR; S18524, S18524.

InterPro; IPR002173; PfkB.

Pfam; PF00249; PfkB.

PROSITE: PS00583; PFKB_KINASES_1; 1.

PROSITE: PS00584; PFKB_KINASES_2: 1.
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nes 81; Conserv
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

November 24, 2002, 23:11:44; Search time 95 Seconds (without alignments) 1034.573 Million cell updates/sec Run on:

US-09-912-020-325 2393 1 MKVTLPEFERAGVMVVGDVM......FEDGCSTTNIIKKIQQDKKG 477 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 segs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL_21:*

1: Sp_archea:*
2: Sp_bacteria:*
3: Sp_fungi:*
4: Sp_human:*
5: Sp_lnvertebrate:*
6: Sp_mammal:*
7: Sp_mhc:* sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:*
sp_vorrebrate:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. sp_rvirus:* sp_bacteriap:* sp_archeap:*

sp_unclassified:*

SUMMARIES

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ion	O8xbm4 escherichia	almonella	Q8xew9 salmonella	almonella	almonella	yersinia	pasteure]	Oghug9 pseudomonas	148046 haemophilus	caulobact	campylob	Q98154 rhizobium l	9x5i8 neisseria m	neisseria	Q9jrj4 neisseria m	ralstonia
Description	O8xpm4	09aj74 s	Q8xew9	Ogrfy8 s	09rfy7 s	08z160	99cme6	69hnd60	048046 h	09a2c5	Q9pne5	098154	09x5i8 n	09k004	Q9jrj4	0870x9
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ID	Q8XBM4	29AJ74	Q8XEW9	29RFY8	29RFY7	082160	Q9CME6	69HH60	248046	Q9A2C5	Q9PNE5	098154	. 815X6C	Q9K004	Q9JRJ4	08Y0X9
	16	7	16	7	~	16	16	16	7	16	16	16		16	16	16
% Query Watch Length DB	477	477	477	477	473	476	476	474	342	483	461	496	313	323	323	319
% Query Match	99.7	95.1	94.7	94.0	93.0	86.8	71.1	56.4	46.9	37.8	36.1	36.1	31.5	31.5	31.2	30.2
Score	2385	2276	2265	2250	2225	2076	1701	1350.5	1122	904.5	863	863	753.5	753.5	745.5	721.5
Result No.	п	7	e	4	5	9	7	80	6	10	11	12	13	14	15	16

	ໝ	QYZSDS Streptomyce Ogr6eg fusobacteri	-	Q8rf00 fusobacteri	O66572 aquifex aeo	Q51060 neisseria g	Q9jxf0 neisseria m	Q9jwi8 neisserla m	Q8y2m6 ralstonia s	Q43999 alcaligenes	Q8rbp6 thermoanaer		Q9i2f4 pseudomonas	Q9x055 thermotoga	Q917r2 salmonella	Q8rd45 thermoanaer	6	Q9uz37 pyrococcus	~	Q982u3 rhizoblum l	Q9a9m6 caulobacter	Q8z2w9 salmonella	Q944f4 oryza sativ	Q8ult9 pyrococcus	058466 pyrococcus	Q9shh5 arabidopsis	Q8y0n0 ralstonia s
Q9WWX7	OSFBII	QYZOBS	066836	Q8RF00	066572	051060	Q9JXF0	09JWI8	Q8Y2M6	043999	Q8RBP6	Q9KBR8	Q912F4	Q9X055	09L7R2	Q8RD45	Q8R1Q9	Q9UZ37	Q8YW32	0982U3	Q9A9M6	Q822W9	Q944F4	Q8U1T9	058466	Q9SHH5	Q8YONO
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28.4	25.5	24.8	23.6	17.0	16.4	15.4	14.6	14.2	13.1	13.0	9.3	8.4	8.2		8.0	8.0	7.9	7.9	7.9	7.7		•	7.7	7.6	7.6	7.6	7.6
678.5	610.5	784 784	64	407.5	391.5	368.5	348.5	340.5	314	311.5	221.5	201.5	197	194	192.5	190.5	190	189.5	188	185	184.5	183.5	183.5	182.5	181.5	181.5	181
17	B 6	20	21	22	23	24	22	56	27	28	58	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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RRAE.
Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jin U.-H., Chung T.-W., Kim C.-H.;
"ADP-heptose synthase (rfaE) gene of salmonella typhimurium.";
submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF155126; AAK20933.1;
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                                                                                                                                                                                  Length 477;
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A: 51064 MW; BB877FEF6636E67C CRC64;
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                            99.7%; Score 2385; DB 16; 99.6%; Pred. No. 2.1e-142; ive 1; Mismatches 1;
InterPro; IPR004821; Cyt_tran_rel.
InterPro; IPR002173; PfkB.
Pfam; PF01467; Cytidylyltransf; 1.
Pfam; PF00294; PfkB; 1.
TIGRFAMS; TIGR00125; Cyt_tran_rel; 1.
PROSITE; PS00583; PFKB_KINASES_1; UMKNOWN_1.
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Pfam: PF00294; pfkB; 1.
TGRFAM: TIGRO0125; Cyt.tran_rel; 1.
PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_1.
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InterPro; IPR004820; Cytidylyltransf.
InterPro; IPR004821; Cyt_tran_rel.
InterPro; IPR002173; PfkB.
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01-JUN-2001
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01-JUN-2002
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Matches 475;
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D., Wain J.,
                                                                                                                                                                                                                                                                                                 TDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES—S. typhimurium; STRAIN-LT2 / SGSC1412 / ATCC 700720; MEDILE—21534948; PubMed=11677609; MCClelland M. Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courthey L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                       61 ASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPT1TKLRVLSRNQOLIRLD 120
                                                                                                                                                                                                                                                                                                                                                                        FEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STVSPIELENAVRGRADTGFGVMTEEELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL 360
                                                                                                                            Gaps
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Salmonella typhi.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Bifunctional, putative sugar nucleotide transferase domain
ADP-L-glycero-D-manno-heptose synthase (EC 2.7.-..) (ADP-he
RFAE OR STM3200 OR STY3379.
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                         51169 MW; 269475F3FF9EB9EF CRC54;
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MEDLINE-21534947; PubMed-11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R.,
                                                                    Score 2276; DB 2;
Pred. No. 1.6e-135;
); Mismatches 10;
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93.9%;
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Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis R., Dowd L., Whitele, Farrar J., Feltwell T., Hamlin W., Haque A., Hien T.T., Holreiw, Farrar J., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Moule M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; a multiple drug resistant Salmonella T. Complete genome sequece of a multiple drug resistant Salmonella T. Therrica serovar Typhi CT18."; anterica serova
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella.
NCBI_TaxID=28901;
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477 AA; 51124 MW; E4FF6BIDEE80568C CRC64;
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Last annotation update)
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Matches 445; Conservative
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01-MAY-2000 (
01-JUN-2002 (
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"The rfaE gene from Escherichia coli encodes a bifunctional protein involved in the biosynthesis of the lipopolysaccharide core precursor ADP-L-glycero-D-manno-heptose.";
J. Bacteriol. 182:488-497(2000).
EMBL: AFIG5661; AAD49846.1; -.
HSSP; P27623; 1COZ.
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92.9%; Pred. No. 7e-134;
ive 20; Mismatches 14; Indels
                    Valvano M.A., Marolda C.L., Bittner M., Glaskin-Clay M., Klena J.D.;
                                                                                                                                                                                              InterPro; IPR004820; Cytidylyltransf.
InterPro; IPR004821; Cyt_tran_rel.
InterPro; IPR002173; PfkB.
Pfam; PF00467; Cytidylyltransf; 1.
Pfam; PF00294; pfkB; 1.
TIGRFAMS; TIGR00125; Cyt_tran_rel; 1.
PROSITE: PG00583; PFKB KINASEZ 1; UNKNOWN 1.
SEQUENCE 477 AA; 51119 MW; 9215BA18BD655FF7 CkC54;
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MEDLINE=20096694; PubMed=10629197;
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MEDLINE=20096694; PubMed=10629197;
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Bacteria; Proteobacteria;
Salmonella.
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Best Local Similarity 92.99
Matches 442; Ccnservative
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Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamilin N., Holroyd S., Jagels K., Karlyshev A.V.,
A. Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
A. Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
T. Genome sequence of Yersinia pestis, the causative agent of plague.";
Mature 413:523-57(2001).
B. Mature 413:523-57(2001).
R. InterPro; IPR004820; Cytidylyltransf.
R. InterPro; IPR004820; Cytidylyltransf.
R. InterPro; IPR004820; Cytidylyltransf.
R. Pfam, PF01467; Cytidylyltransf; 1.
R. Pfam, PF01467; Cytidylyltransf; 1.
R. Pfam; PF004034; PfkB.1.
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
                                                                                                                                                                                                                                                                                                                           Length 476;
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                                                                                                                                                                                                                                                                        Transferase; Complete proteome.
SEQUENCE 476 AA; 51218 MW; E68FF382DC892636 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                       TIGRFAMS; TIGR00125; cyt_tran_rel; 1.
PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_1.
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STRAIN-PM70;
MEDLINE-21145866; PubMed=11248100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2002 (TrEMBLrel. 21,
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 Valvano M.A., Marolda C.L., billing.
Klena J.D.;
"The riag gene from Escherichia coll encodes a bifunctional protein involved in the biosynthesis of the lipopolysaccharide core precursor J. Bacteriol. 182:488-497 (2000).

EMBL; AFIGS62; AAD49447.1: --
INTERPO; IPRO04820; Cytidylyltransf.
InterPro; IPRO04820; Cytidylyltransf.
InterPro; IPRO04821; Cyt.tran_rel.
InterPro; IPRO04121; Cyt.tran_rel.
InterPro; IPRO04173; PfkB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ASLGANARLYGLTGIDDAARALSKTLAEVNVKCDEVSVPTHPTITKLRVLSRNQQLIRLD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 TDFERYRGATLLTPNLSEFEAVAGKCKSEDELVERGMKLIADYDLSALLVTRSEQEMTLL 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STAIN-CO-92 / BIOVAR ORIENTALIS;
MEDLINE-21470413; PubMed-11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 473;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ADP-heptose synthase (EC 2.7.-.).
RFAE OR PPO0654.
Yersinia pestis.
                                                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                                                       93.0%; Score 2225; DB 2;
92.2%; Pred. No. 2.6e-132;
ive 20; Mismatches 13;
                                                                                                                                                                                   Pfam; PF01467; Cytidylyltransf; 1.
Pfam; PF00294; pfkB; 1.
TIGRRAMs; TIGR00125; Cyt_tran_rel; 1.
PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_1.
PRRANT 236 236 E > G.
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                                                                                                                                                                                                                                                                          473 AA; 50868 MW;
                                                                                                                                                                                                                                                                                                                                          Matches 439; Conservative
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, Saier M.H., Hancock R.E.W., Lory S., Olson M.V. genome sequence of Pseudomonas aeruginosa PAO1,
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                                                       opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004912; AAG08381.1;
HSSP; P27623; 1C02.
                                                                                                                                                                                                                                                                                                                                                                                                 274; Conservative
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01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
ADP-heptose synthase.
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             Reizer J., "Complete 9
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Q48046;
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Matches
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STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed-10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrook Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
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                                                                                                                                                                                                                                                                                                                Length 476;
                                 Pm70.";
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                                                                                                                                                                                                                                                                    476 AA; 51884 MW; C4137ECC7B2F02D1 CRC64;
May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam "Complete genomic sequence of Pasteurella multocida Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001). EMBL: AE006127; ARK02968.1; HSSP: P27623; 1CC2.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
LPS biosynthesis protein RfaE.
                                                                                                                                                                                                                                                                                                         Query Match 71.1%; Score 1701; DB 16; Best Local Similarity 69.7%; Pred. No. 2.9e-99; Matches 327; Conservative 65; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            474 AA
                                                                                                                                                                              Pfam: PF01467; Cytidylyltransf; 1.
Pfam: PF00294; pfkB; 1.
TIGREAMs; TIGR00125; cyt_tran_rel; 1.
                                                                                                                InterPro; IPR004820; Cytidylyltransf.
InterPro; IPR004821; Cyt_tran_rel.,
InterPro; IPR002173; PfkB.
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180 KDFAIYRGASLITPNLSEFFTIVGRCADEAELVAKGQALMSELDLGALLVTRGEHGMTLL 239
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MEDLINE-96070820; PubMed-7592970;
Lee N., Sunshine M.G., Engstrom J.J., Gibson B.W., Apicella M.A.;
"Mutation of the htrB locus of Haemophilus influenzae nontypeable strain 2019 is associated with modification of lipid A and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.4%; Score 1350.5; DB 16; Length 474; 57.9%; Pred. No. 3.7e-77; ive 70; Mismatches 128; Indels 1;
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
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Last annotation update)
                                                                                                                                                                                       InterPro: IPR004820; Cytidylyltransf.
InterPro: IPR004821; Cyt_tran_rel.
InterPro: IPR00213; PfkB.
Pfam: PF00467; Cytidylyltransf; 1.
Ffam: PF00294; PfkB: 1.
TIGRRAMs; TIGR00125; cyt_tran_rel; 1.
PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_1.
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SEQUENCE FROM N.A.

STRAIN-ATCC 19089 / CB15;

MEDLINE-21173698; PubMed-11259647;

MEDLINE-21173698; PubMed-11259647;

MISTIME N.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

M. Nierman W.C., Feldblyum T.V., Alley M.R.K., Ohta N., Maddock J.R.,

M. Bisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Detocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

M. Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haff D.H.,

M. Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

M. Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

R. Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

M. Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. US.A. 98:4136-4141(2001).

M. HSSP; Q9TVW2; 1DGY.
                                                                                                           MEDLINE-95172727; PubMed-7868252; Lee NG., Subshine M.C., Apicella M.A.; Lee NG. Clar cloning and characterization of the nontypeable Haemophilus influenzae 2019 rfaE gene required for lipopolysaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 GVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKGTDFERY 186
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Caulobacter.
NCBI_TaxID=155892;
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                                                                                                                                                                                                                                                                                                                                                                                                                 59; Indels
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                  46.9%; Score 1122; DB 2;
67.2%; Pred. No. 5.8e-63;
Live 47; Mismatches 59;
phosphorylation of the lipooligosaccharide.";
J. Biol. Chem. 270:27151-27159(1995).
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01-JUN-2001 (TrEMBLrel. 17, Last sequ
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Infect. Immun. 63:818-824(1995).
EMBL: U17642: AAC43516.1; -.
Interpro: IPR002173; PfkB.
Pfam: PF00294; pfkB: 1.
SEQUENCE 342 AA; 37538 MW; 4:
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ELENAIHARPETGFGIMSEAELK 329
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217; Conserv
                                                              SEQUENCE FROM N.A.
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Matches
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STRAIN-NCTC 11168;
MEDLINE-20150912; PubMed-10688204;
MEDLINE-20150912; PubMed-10688204;
MEDLINE-20150912; PubMed-10688204;
Barkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Ouail M.A., Ralyandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
The genome sequence of the food-borne pathogen Campylobacter jejuni
nature 403:665-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                                           5 LPE-FERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERFGGAANVAMNIASL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                               Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
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                                                                                                                                                                                                                                  483 AA; 49621 MW; 9CD4ED6CD784608A CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Putative ADP-heptose synthase.
                        InterPro; IPR004821; Cyt_tran_rel.
InterPro; IPR002173; PfkB.
Pfam; PF00294; pfkB; 1.
TIGRFAMS; TIGR00125; cyt_tran_rel; 1.
PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_1.
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InterPro; IPR004820; Cytidylyltransf.
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Matches 214; Conservative
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                                                                                                                                                                                                                                                                                                                              9 ERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANAR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGATLLTPNLSEFEAVVGKCKTEEEIVERGM-KLIADYELSALLVTRSEQGMSLLQPGKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGTSTVSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                       20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 461;
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                 461 AA; 51237 MW; 490D9FDB4EB58322 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                          36.1%; Score 863; DB 16; ilarity 43.1%; Pred. No. 2e-46; Conservative 90; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   496 AA.
                                                             InterPro; IPR004821; Cyt_tran_rel.
InterPro; IPR002173; PfkB.
Pfam; PF01467; Cytidylyltransf; 1.
Pfam; PF00294; pfkB; 1.
TIGRFAMS; TIGR00125; Cyt_tran_rel; 1.
EMBL; AL139077; CAB73404.1; -.
HSSP; P27623; 1CO2.
InterPro; IPR004820; Cytidylyltransf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-MAFF303099;
MEDLINE-21082930; Pubmed-11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 18, C
(TrEMBLrel. 18, I
(TrEMBLrel. 21, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP-heptose synthase.
                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                          Complete proteome.
SEQUENCE 461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-381;
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01-JUN-2002
                                                                                                                                                                                                                                                                                     Matches 203;
                                                                                                                                                                                                                                            Query Match
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||||||||| :: || |: || :: || || 309 VVVGKRGTARLIYVEELEGALFGALFRSHGPTAHKDAILDASSAARWVAAWKEEGLSVGFTNGCF 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAG 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 ANARLVGLFGIDDAARALSKSLADVNVKCDFVSVPT-HPTITKLRVLSRNQQLIRLDFEE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 GFEGVDPQ?LHE-----RINQALSSIGALVLSDYAKGALAS--VQQMIQLARKAGVP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLIDPKGTDFERYRGATLLTPNLSEFEAVVGKCK-TEEEIVERGMKLIADYELSALLVTR 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250 SEKGMSVVGPDEA-RHIATQAREVFDVSGAGDTVIATFALALASGADPVAAASIANAAGG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   410 VSFEEDTPQRLIAGILPDLLVKGGDYKPEEIAGSKEVWANGGEVLVLNFEDGCSTTNIIK 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 VVVGKLGTSTVSPIELENAV-RGRADTGF--GVMTEEELKLAVAAARKRGEKVVMTNGVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DILHAGHVSYLANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWV
                                                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                        Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
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Kahler C.M., Stephens D.S.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF125564; AAD32179.1; -.
InterPro: IPR002173; PfkB.
Pfam; PF00294; pfkB; 1.
PROSTIF: PS00583; PFKB.KINASES_1; UNKNOWN_1.
                                                                                                                                                                                      496 AA; 51449 MW; 49DB1E271653AA76 CRC64;
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(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                      tch 36.1%; Score 863; DB 16; al Similarity 43.3%; Pred. No. 2.2e-46; 209; Conservative 69; Mismatches 183;
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InterPro; IPR004820; Cytidylyltransf.
InterPro; IPR004821; Cyt_tran_rel.
InterPro; IPR002173; PfkB.
Pfam; PF01467; Cytidylyltransf; 1.
Pfam; PF00294; pfkB; 1.
IIGRFAMS; TIGR00125; Cyt_tran_rel; 1.
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                                                                                                                                                             Complete proteome. SEQUENCE 496 AA;
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01-NOV-1999
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SEQUENCE
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MEDLINE-20179755; PubMed=10710307;

MEDLINE-20179755; PubMed=10710307;

MELGELIN H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Clecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.K., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;

"Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                 : :: : : | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: |:: | |:: |:: | |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 VDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKGTDFERYR 187
                                                                                                                                                                                                                                                                                                                                                                                                                    GATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLLQPGKAPL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 HMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGTSTVSPIE 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=491;
                                                                                                   Gaps
                                                                                                                                                                                                                                    68 RLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFEEGFEG 127
                                                                                                                                                                    8 FERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 FERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 FAQAKVLVVGDVMLDRYWFGDVSRISPEAPVPVAKIGRIDQRAGGAANVARNIASLGGRA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 323;
                                                 DB 2; Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49; Mismatches 100; Indels
                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            323 AA; 34998 MW; FF1B490F54E79D97 CRC64;
  E940F9CC3786EA15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16;
                                             31.5%; Score 753.5; DB 2;
51.5%; Pred. No. 8.8e-40;
iive 49; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.5%; Score 753.5; DB 1
51.5%; Pred. No. 9.2e-40;
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PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_1.
Complete proteome.
SEQUENCE 323 AA; 34998 MW; FF1B490F54E79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 323 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP-heptose synthase, putative.
    33833 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 287:1809-1815(2000).
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TIGR; NMB0825; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002173; PfkB.
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                                                                                               Conservative
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Best Local Similarity
    313 AA;
                                                                     Local Similarity
nes 159; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308 LENAVRGRA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303 LIKALSGQS 311
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01-DEC-2001
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    SEOUENCE
                                                 Query Match
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Q9K004
                                                                                               Matches
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SEQUENCE FROM N.A.
STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
MEDLINE=20187481; PubMed=10722605;
Klee S.R., Nasslf X., Kusecek B., Merker P., Beretti J.L., Achtman M.,
                                   GATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLLQPGKAPL 247
                                                                                                                                                                                                                                                                                                                                                                       248 HMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGTSTVSPIE 307
RLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQOLIRLDFEEGFEG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis (serogroup A), and
Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 FERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
MEDIANE=2022556; PubMed=10761919;
MEDIANE=2022556; PubMed=10761919;
MEDIANE=2022556; PubMed=10761919;
MEDIANE=2022556; PubMed=10761919;
MEDIANE=2022556; PubMed=10761919;
MEDIANE=2022556; PubMed=20, Bentley S.D., Churcher C.,
Bayes R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd & Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Slmmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.,
"Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                    VDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKGTDFERYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09.07.7.
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Putative DP-heptose synthetase (EC 2.7.) (Putative ADP-heptose-
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323 AA; 35124 MW; 044C34579F719370 CRC64;
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50.5%; Pred. No. 2.9e-39;
iive 49; Mismatches 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00294; pfkB; 1.
PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_1
Transferase; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=65699, 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308 LENAVRGRA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     meningitidis 22491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RFAE OR NMA1034
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Matches 156;
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14 FAQAKVLVVGDVMLDRYWFGDVSRISPEAPVPVAKIGRIDQRAGGAANVARNIASLGGKV 73
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Search completed: November 24, 2002, 23:18:30 Job time: 98 secs

308 LENAVRGRA 316 1 |: |:: 313 LTKALSGQS 321

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Gencore version 5.1.3

Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 24, 2002, 23:14:19; Search time 37 Seconds

(without alignments)
379:317 Million cell updates/sec
Ly393
Sequence: 1393
Sequence: 1393
Sequence: 2393
Seconds (appext 0.5
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 262574 seqs, 29422922 residues
Total number of hits satisfying chosen parameters: 262574
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Database: Issued_Patents_AA:*

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3: /cgn2_6/ptcdata/2/iaa/6A_COMB.pep:*

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5: /cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTE

	Description	Sequence 4521, Ap		5583,	2, App	10,	4	281	8	7	ý	e,	'n	7		390		33	6, 1	34,	2, 2	7	7	7	7,	'n	32,	4, 7
SUMMARIES	ΔI	US-09-134-001C-4521	US-09-134-001C-5560	US-09-134-001C-5583	8-80-	US-08-804-227C-10	US-08-804-198-4	US-09-199-637A-281	US-08-479-614-8	US-08-479-614-2	-08-856-	US-08-955-957A-3	US-08-961-539-2	US-09-185-826-2	US-08-479-614-5	US-09-134-001C-3900	US-09-320-878-2	US-09-105-537-33	US-09-105-537-6	US-09-091-097-34	US-08-461-722-2	US-08-336-251-2	PCT-US94-06362-2	US-09-428-517-2	US-08-627-873-7	US-08-116-098-2	US-08-687-590-32	US-08-790-912-4
	DB	4	4	4	٣	7	7	4	~	7	m	4	7	4	~	4	٣	4	4	4	4	4	ស	4	7	-	4	7
	Query Match Length	315	137	312	347	3724	3724	859	362	361	328	366	303	303	345	321	3739	3739	11877	207	547	547	547	4150	1056	552	552	1861
de	Query Match	6.9	6.3	5.7	5.7	5.6	5.6	5.4	4.9	4.9	4.8	4.8	4.7	4.7	4.7	4.6	4.6	4.6	4.6	4.5	4.4	4.4	4.4	4.3	4.3	4.3	4.3	4.3
	Score	165.5	150	137.5	137.5	134.5	134.5	130	117.5	116.5	116	115.5	112.5	112.5	111.5	110	110	110	110	107.5	106	106	106	104	103.5	102.5	102.5	102
	Result No.	П	7	m	4	S	φ	7	6 0	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

Sequence 12, Appl	Sequence 12, Appl	Sequence 2, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 5, Appli	Sequence 450, App	Sequence 454, App	Sequence 12, Appl	Sequence 6, Appli	Sequence 4, Appli	Sequence 4, Appli							
US-09-222-817-12	US-09-222-786-12	US-09-144-085-2	US-08-804-227C-3	US-09-144-085-1	US-09-335-409-5	US-09-568-102-5	US-09-567-969-5	US-09-568;480-5	US-09-568-486-5	US-09-568-472-5	US-09-567-899-5	US-09-071-035-450	US-09-071-035-454	US-08-804-227C-12	US-08-804-198-6	US-07-642-734C-4	US-08-439-009A-4	
9	4	5	7	7	3	4	7	7	4	4	4	3 4	3	7	7	2	7	
530	53(6095	186	508	725	725	725	725	725	725	725	131	131	189	189	356	3567	
4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	
101.5	101.5	101	100	100	100	100	100	100	100	100	100	99.2	99.5	99.5	99.5	99.5	99.5	
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

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RESULT 1 US-09-134-001C-4521 US-09-134-001C-4521 US-09-134-001C-4521 Sequence 4521, Application US/09134001C Sequence 4521, Application US/09134001C Sequence 4521, Application US/09134001C Sequence 4521, Application US/09134 Sequence 4521, Application US/09/194 Sequence 4521, Application US/09/194 TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US 60/064,964 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 SEQ ID NO 4521 LENGENT: 315 LENGENT: 315 TYPE: PRT ORGANISM: Staphylococcus epidermidis US-09-134-001C-4521
Query Match 6.9%; Score 165.5; DB 4; Length 315; Best Local Similarity 22.6%; Pred. No. 3.1e-08; Matches 77; Conservative 56; Mismatches 142; Indels 65; Gaps 13;
QY 2 KVTLPEFERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMN 59 11
QY 60 IASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRL 119
QY 120 DFEEGREGVDPQPLHERINQALSSIGALVLSDYAKGALASVQ 161 :
QY 162 QMIQLARKAGVPVLIDPKGTDFERYRGATLLTPNLSEFEAVVGKCKTEE 210
QY 211 EIVERGMKLIADYELSALLVTRSEQGMSLLQPGRAPLHMPTQAQEVYDVTGAGDTVIGVL 270 :: : Db 211 SDWKETATYFLDLGISAVLITLGEQGTYCAYQEQYKM-IPACNVKAIDTTAAGDTFIGAF 269
QY 271 AATLAAG-NSLEEACFFANAAAGVVVGKLGTSTVSPIELE 309 : :: : D 270 LSELNKDLSNLESAIRLANQASSLTVQRKGAQASIPTRKE 309

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153 IAQITEKTGAQLVVDAEKDLVETVLPYR-PLFIKPNKDELEVMFNTTVKSDEDVIKYGKE 211
                                                                                                                                                                                            72 LTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLR---------VLSRN---QQL 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRESELDVDLIKKATIFHYGSISLIDEPCRST...---HLAAMDIAKRSGSILSYDP 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 MIQL-----ARKAGVPVLIDPKGTDFERYRGATLLTPNLSEFEAVVG-KCKTEEEIVE 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 VVCFGEMLID---FIPT-----VAGVSLAEAPAFEKAPGGAPANVAVCISKLGGSSAFIG 79
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MIQLARKAGVPVLIDPKGTDFER---YRGATLLTPNLSEFEAVVG-KCKTEEEIVERGMK
                                                                                                                                                  LIADYELSALLVTRSEQGMSLLQPGKAPLHMPTQA----QEVYDVTGAGDTVIGVLAATL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ranayama, Yoshinori
APPLICANT: Ranayama, Yoshinori
TITLE OF INVENTION: Fructokinase Genes and Their Use in
TITLE OF INVENTION: Metabolic Engineering of Fruit Sweetness
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 347;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.7%; Score 137.5; DB 3; Best Local Similarity 24.4%; Pred. No. 2.4e-05; Matches 85; Conservative 48; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  023070-077400US
                                                                                                                                                                                                                                                                                                                                          275 AAGNSLEEACFFANAAAGVVVGKLGTST 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/826,611
FILING DATE: 05-APR-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Bastian, Kevin L.
REGISTRATION UNUBER: 34,774
REFRENCE/DOCKET UNMBER: 0230:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08826611 Patent No. 6031154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 347 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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MOLECULE TYPE: protein
US-08-826-611-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-826-611-2
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                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn BARNIOS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR PILING DATE: 1997-10-8
PRIOR FILING DATE: 1997-10-8
PRIOR FILING DATE: 1997-10-8
RIOR FILING DATE: 1
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID ANNO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR SPOLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401 GALEAVDWVVSFEEDTPQRL--IAGILPDLLVKGGDYKPEEIAGSKEVWANGGEVLVLNF 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 GGAANVAMNIASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVL 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 LKSGQ-----ETEINAPGPKVTHAQFEQLLSQIRRTTNDDIVIVAGSVPNSIPSDAYAQ 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 GKGINVSRVLKTLDVDSTALGFSG-GFPGDFIAQTLEDSNIQSDFVQVDED---TRINVK 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 150; DB 4;
Pred. No. 2.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5583, Application US/09134001C Patent No. 6380370
                                                                     Sequence 5560, Application US/09134001C Patent No. 6380370
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Best Local Similarity
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Best Local Similarity
Matches 58; Conserv
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US-09-134-001C-5583
                                  US-09-134-001C-5560
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1439 ELTAQSGHKRHATLLRLVRAHAAAVLGQSSGDAVS----SARAFRDLGFDSLTALELR 1492
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                                                                                                                                                              -KLAVAAARKRGEKVVMTNGVFDILHAGHVSYLANARKLGDRLIVAVNSDASTKRLKGDS 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 VGLTGI------DDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFE 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 RAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANARL 69
                                                                    271 AATLAAGNSLEEACF-FANAAAGVVVGKLGTSTVSPIELENAVRGRADTGFGVMTEEEL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 111;
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                                                                                                                                                                                                                                                                                    RPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRLIAGILPDLLVKGGD 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rao, Nagaraja R.
APPLICANT: Richardson, Mark A.
APPLICANT: Rosteck, Paul R., Jr.
ITILE OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: Macintosh 7.0 SOFTWARE: Microsoft Word 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/804,198
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08804198 Patent No. 5945320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Burgett, Stanley G. APPLICANT: Kuhstoss, Stuart A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: P9
TELEOMAUNICATION INFORMATION:
TELEPHONE: 317-276-3885
INFORMATION FOR SEO ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
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CITY: INDIANAPOLIS
STATE: IN
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1332 AAGVPAFSVAWSPWAGGTPADGAEAEFLSRRGLAPLDPD----QAV----RTLRRMLERG 1383
                                                                                        --LKRLFHPNLKLLLVTEGSAGCRYYTKEFKGR----VNSIKVKAVDTTGAGDAFTGGVL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 VGLTGI-----DDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGFEG--VDPQPLHERINQALSSIGALVLSDYAKG------ALASVQQMIQLAR 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MK--LIADYELSALLVTRSEQGMSLLQPG----KAPLHMPTQAQEVYDVTGAGDTVIGVL 270
--- MSVWNLADIIKISEDEISFLTGADDPNDDEVV- 238
                                            RGMKLIADYELSALLVTRSEQGMSLLQ---PGKAPLHMPTQAQEVYDVTGAGDTVIGVLA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANARL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---IDPKGTDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERG
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                                                                                                                                      ATLAAGNS-----LEEACFFANAAAGVVVGKLGTSTVSPIELENAVR 313
                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 134.5; DB 2;
; Pred. No. 0.0026;
48; Mismatches 196;
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: DeHOFF, Bradley S.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Kosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
APPLICANT: SUTTON, Kimberly L.
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08804227C Patent No. 5876991
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/ACENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-82:
TELECOMMUNICATION INFORMATION:
TELEPHORE: 317.276.2459
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCI(DOS) Text only CURRENT APPLICATION DATA:
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COMPUTER: IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 24.0%
Matches 112; Conservative
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NLRLPLWPSEDAARSGI-
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                                                                                                                                                                                             1439 ELTAQSGHKRHATLLRLVRAHAAAVLGQSSGDAVS-----SARAFRDLGFDSLTALELR 1492
                                   1332 AAGVPAFSVAWSPWAGGTPADGAEAEFLSRRGLAPLDPD----QAV----RTLRRMLERG 1383
                                                                                                                  1384 SACGAVADVEWS-----RFAASYTWVRPAVLFDDIPDVQRLRAAELAPSTGDSTTSELVR 1438
                                                                                                                                                         271 AATLAAGNSLEEACF-FANAAAGVVVGKLGTSTVSPIELENAVRGRADTGFGVMTEEEL- 328 '
                                                                                                                                                                                                                                                               MK--LIADYELSALLVTRSEQGMSLLQPG----KAPLHMPTQAQEVYDVTGAGDTVIGVL 270
                                                                                                                                                                                                                                        -KLAVAAARKRGEKVVMTNGVFDILHAGHVSYLANARKLGDRLIVAVNSDASTKRLKGDS 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 LSKS-----LADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFE------EGFEGVD 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 PQPLHERINQALSSIGALVLSDYAKGAL-----ASVQQMIQL--ARKAGVPVLIDPKG 180
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----IDPKGTDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERG 216
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                                                                                                                                                                                                                                                                                                                                            APPLICANT: Mahajan-Miklos, Shalina
APPLICANT: Tan, Man-Wah
APPLICANT: Tan, Man-Wah
APPLICANT: Tan, Man-Wah
APPLICANT: Drenkard, Eliana
APPLICANT: Trangalis, John
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REPERENCE: 00786/361002
CURRENT APPLICATION NUMBER: US/09/199,637A
FRIOR APPLICATION NUMBER: US/09/199,637A
FRIOR PELING DATE: 1998-11-25
FRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
                                                                                                                                                                                                                                                                                                                     RPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRLIAGILPDLLVKGGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 130; DB 4;
Pred. No. 0.00062;
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5.4%; Score 130; DB
Best Local Similarity 23.8%; Pred. No. 0.000
Matches 123; Conservative 75; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 281, Application US/09199637A Patent No. 6355411
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Mahajan-Miklos, Shalina
Tan, Man-Wah
Cao, Hui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Pseudomonas aeruginosa
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Goodman, Howard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
169 KAGVPVL--
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APPLICANT:
                                                                                                                                                                                                                                                                                                                     388
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                                                                                                                                                                                                                                                            305 KPA------LARGELHCVGATTLDEYRQYIEKDAALERRFQKVIVDEPSEEDTIAIL 355
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                                                                                                                                                                                                        334 AARKRGEK----VVMTNGVFDILHAGHVS--YLANARKLGDRLIVAVNSDASTKRLKGDS
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CORRESPONDENCE ADDRESS:
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Pred. No. 0.0026;
55; Mismatches 145;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 937-4884
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FILING DATE: June 7, 1995
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Patent No. 5861294
GENERAL INFORMATION:
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19.08;
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Best Local Similarity 19.08
Matches 70; Conservative
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TOPOLOGY: linea.
TECHLE TYPE: protein
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-479-614-8
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-----ARKAG 171
                                                                                                                                                                       172 VPVLIDPKGTDFERYRGATLLTP--NLSEFEAVVGKCKTEEEIVERGMKLIADYELSALL 229
                                                                                                                                                                                                                                                         F-----ETKDIKEIARKTQALPKVNSKRQRTVIFTQGRDDTIVATG-----NDVTAFP 299
                                                                                                                                                                                                                                                                                              230 VTRSEQGMSj.LQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANA 289
                                                                                                                                                                                                                                                                                                                       72 FKVEYHAGGSTQNSMKVAQWMIQEPHRAATFFGCIGIDKFGEILKSKAADAHVDAHYYEQ 131
                                                                                                           132 NEOPTGTCAACITGGNRSLVANLAAANCYKKEKHLDLENNWMLVEKARVYYIAGFFLTVS 191
44 NTIEERPGGAANVAMNIASLGAN-----ARLVGLTGIDDAARALSKSLADVNVKCDFVSV 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bennett, Alan B.
APPLICANT: Kanayama, Yoshinori
TITLE OF INVENTION: Metabolic Engineering of Fruit Sweet
                                                                                                                                                130 PQPLHERINQALS----SIGALVLSDYAKGALASVQQMIQL---
                                                                       99 PTHPTIT-KLRVLSRNQQLI-------RLDFEEG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; DB 3;
0.0031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         023070-077400US
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Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/826,611
FILING DATE: 05-APR-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.8%; Scc.
23.7%; Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR EEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08826611 Patent No. 6031154 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-826-611-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                    300 VLDQNQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                         290 AAGVVVGKLG 299
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342 AASVIIRRTG 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Simmatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-826-611-6
                                                                                                                                                                                                                                                         252
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 --FEGVD 129
                                                                                              172 VPVLIDPKGTDFERYRGATLLTPNL-SEFEAVVGKCKTEEEIVERGMKLIADYELSALLV 230
                                                                                                                                                                     253 F-----ETKDIKEIAKKTQALPKMNSKRQRIVIFTQGRDDII-----MATESEVTAFAV 301
                                                                                                                                                                                                                     231 TRSEQGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAA 290
                                                                                                                                                                                                                                            133 NEQPTGTCAACITGDNRSLIANLAAANCYKKEKHLDLEKNWMLVEKARVCYIAGFFLTVS 192
                                                                       130 PQPL-----HERINQAL--SSIGALVLSDYAKGALASVQQMIQL-----ARKAG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKVTLPEFERAGVM-----VVGDVMLDRYWYGPTSRISPEAP----VPVVKV 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cowart, Marlon Daniel, Halbert, Donald N., APPLICANT: Kerwin, Dr., James F., McNally, Teresa TITLE OF INVENTION: Adenosine Kinase Polypeptides NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153;
99 PTHPTIT-KLRVLSRNQQLI------RLDFEEG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.9%; Score 116.5; DB 20.3%; Pred. No. 0.0032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSEE: Abbott Laboratories
T: D-377 AP6D, 100 Abbott Park Road
Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPPERATING SYSTEM: Macintosh System 7.1 SOFTWARE: Microsoft Word 6.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/479,614 FILING DATE: June 7, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5749.US.DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette, 3.50 inch COMPUTER: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08479614 Patent No. 5861294 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Thomas D. Brainard
REGISTRATION NUMBER: 32,459
REFERENCE/DOCKET NUMBER: 574
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (708) 937-4884
TELEFAX: (708) 938-2623
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
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ADDRESSEE: Abbott La
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nes 75; Conserva
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                                                                                                                                                                                                                                                                                            291 AGVVVGKLG 299
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                                                                                                                                                                                                                                                         302 LDQDQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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144 IGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPK-----GTDFER--YRGATLLTPN 195
                                                                                                         254 Q-EVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGTSTVSPIELENAV 312
                                                                                                                                                                                                       247 DVPVVDPTGIGAAFRAGFLAGAGRGLSIVSA----ARLGCVLAARALGTVGPADLPDRS 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFEEGFEGVDP-- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 VRLDQVKVGSVNRMDSD------DKFAGGKGINVSRVLKRLNISNT-ATGFIGGF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 VMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGG-AANVA-----MNIASLGANARLVGL 72
                                     144 ---LICPD---DPAAMVRHTAQ-CREPGLPFVADPSOOLARLETDEVRALVHGAHWVFTN
                                                                                 196 LSEFEAVVGKCKTEEEIVER-GMKLIADYE-LSALLVTRSEQGMSLLQPGKAPLHMPTQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.7%; Score 112.5; DB 2; Best Local Similarity 23.5%; Pred. No. 0.0061; Matches 76; Conservative 54; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEG for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/961,539
                                                                                                                                                                                                                                                   313 RGRADIGFGVMTEEELKLAVAAARKRGEKVVMT 345
                                                                                                                                                                                                                                                                                          302 GGSARHGEGRVRRGR----GGAARPRAGRPHMT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Zalacain, Magdalena
APPLICANT: Brown, James R.
TITLE OF INVENTION: No. 5861281el lacC
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert, Price & Rhoads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GM10114
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Patent No. 5861281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
CLASSIFICATION ATA:
APPLICATION NUMBER:
FILING DATE:
TTORNEY/AGENT INFORMATION:
NAME: DICKINSON, Q. TODD
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM10
TELECOMMUNICATION INFORMATION:
TELECHONE: 215/994-2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
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                                                                                                    126 ----EGVDPQPLHERINQALSSIGALVLSDYAKGAL-----ASVQQMIQLARKAGVPVL 175
                                                                                                                                            113 FYRNPSADMLLTPAELN--LDLIRSAKVFHYGSISLIVEPCRAAHMKAMEVAKEAGALLS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95 FVSVPT-HPTITKLRVLSRNQQLIRLDFEEGFE------GVDPQPLHERINQALSS 143
                   67 ARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFEEGF- 125
                                                                                                                                                                                                                  171 YDPNLRLPLWPSAEEAKKQIKSIWDSADVIKVSDVELEFLTGSNKIDD----BSAMSLWHP 227
                                                                                                                                                                                                                                                                       223 YELSALLVTRSEQGMSL----LQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGN 278
                                                                                                                                                                                                                                                                                               71; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 VDGLEVRRGGVAVGIAFGLGRPGPTPLLVGAVGND-----FADYGTWPKEHGVDTG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 VNTIEERPGG-AANVAMNIASLGANARLVGLTGIDDAARALSKSLADV-----NVKCD 94
                                                                                                                                                                                     176 IDP------KGTDFERYRGATLITPNLSEFEAVVGKCKTEEEIVERGMKLIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 115.5; DB 4; Length 366;
; Pred. No. 0.0042;
31; Mismatches 146; Indels 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 46285

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentuR Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/955,957A
                                                                                                                                                                                                                                                                                                                                                          S-----LEEACFFANAAAGVVVGKLGTSTVSPIELE 309
                                                                                                                                                                                                                                                                                                                                                                                                 282 TILEDEARLKEVLRFSCACGAITTTKKGAIPALPTASE 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DeHOFF, Bradley S.
APPLICANT: ROSTECK Jr., Paul R.
TITLE OF INVENTION: SAM OPERON
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
COUNTRY: U.S.
ZID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INCORMATION:
TELEPHONE: 317-276-3334
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 25.5%;
Matches 85; Conservative 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 366 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-955-957A-3
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131 QPLH-ERINQALSSIGA---LVLSDYAKGALASV--QQMIQLARRAGVPVLIDPKG---- 180
                                                                                                                                                                                                                                                           229 LVTRSEQGESLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFAN 288
                                                                                                                                                                                                                                                                                                   -----RELDFEEG-----FEGVDPQPL----HERINQAL--SSIGALV 148
                                                              109 EPVKLEELKAILSSLTAEDTVVFAGSSAKNLGNVIYKDLISLTROTGAQVVCDFEGQTLI 168
                                                                                                                                                                     67 --ARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTIT-KLRVLSRNQQLI----- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 KAATFFGCIGIDKFGEILKRKAAEAHVDAHYYEQNEQPTGTCAACITGDNRSLIANLAAA 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 VVDKDFLDKYSLKPNDQILAEDKHKELFDELVKKFKVEYHAGGSTGKSIKVAQWMIQQPH 81
                                                                                                                                 --TDFERYRGATLLTPNLSEFEAVVG-KCKTEEEIVERGMKLIADYELS------AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5. Application US/08479614
Fatent No. 5861294
Fatent Cowart, James F. McNally, Teresa APPLICANT: Revin, Jr., James F., McNally, Teresa TITLE OF INVENTION: Adenosine Kinase Polypeptides CORRESPONDENCE ADDRESS: ADDRESSE: AD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 undels
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4.7%; Score 111.5; DB 2;
Best Local Similarity 19.2%; Pred. No. 0.0096;
Matches 66; Conservative 51; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: Macintosh System 7.1 SOFTWARE: Microsoft Word 6.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/479,614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   749.US.D1
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CLASSIFICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch
COMPUTER: MACINIOSh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTOREY AGENT INFORMATION:
NAME: Thomas D. Brainard
REGISTRATION NUMBER: 32,459
REFERENCE, DOCKET NUMBER: 5749
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 937-4884
TELEPRAX: (708) 937-4884
TELEPRAX: (708) 937-583
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC-----GTATTFSDDLATA 288
                                                                                                                                                                                                                                                                                                                                                                                         289 AAAGVVVGKLGTSTVSPIELENA 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-08-479-614-5
                                                                                                                             181
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                                                                                                                                                                                                                                                                                                TGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFEEGFEGVDP-- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 QPLH-ERINQALSSIGA---LVLSDYAKGALASV--QQMIQLARKAGVPVLIDPKG---- 180
                                                           EPVKLEELKAILSSLTAEDTVVFAGSSAKNIGNVIYKDLISLTRQTGAQVVCDFEGQTLI 168
                                                                                                                          181 --TDFERYRGATLLTPNLSEFEAVVG-KCKTEEEIVERGMKLIADYELS-----AL 228
                                                                                                                                                           229 LVTRSEQGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFAN 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zalacain, Magdalena
APPLICANT: Zalacain, Magdalena
APPLICANT: Brown, James R.
TITLE OF INVENTION: No. 6171840el lacC
CORRESPONDENCES: 7
CORRESPONDENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stree
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/185,826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/961,539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GM10114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09185826 Patent No. 6171840 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, 0. Todd
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215/994-2252
TELEPHONE: 215/994-2222
                                                                                                                                                                                                                                                                                                                                                                                      289 AAAGVVVGKLGTSTVSPIELENA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 AC-----GTATTFSDDLATA 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 23.55
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESS: single
linear
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
US-09-185-826-2
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APPLICANT: Lynn Doucette-Stamm et al APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: WUGLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS CURRENCE: GTC-007

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-08-14

PRIOR FILING DATE: 1997-108

PRIOR FILING DATE: 1997-108

RIOR FILING DATE: 1997-108-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NOS: 5674
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                                                                                        SEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLLQPGKAPLHMPTQAQEV 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 NARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFEEGF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 EGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKGTD--- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 IFQDDILHFCSVDLIESDMKNAHEKMIEKFESVGGTIVFDPNVRLPLWEDKLECQRTINA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----SEFEAVVGKCKTEEEIVE---RGMKLIADYELSALLVTRSEQGMSLLQ 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 PGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLE------EACFFANAAA 291
142 NCYKKEKHLDLEKNWMLVEKARVCYIAGFFLTVSPESVLKVAHHASENNRIFTLNLSAPF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 KSEMITQLGND------AFGDIIVE------TIEQL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 110; DB 4; Length 321;
; Pred. No. 0.012;
53; Mismatches 109; Indels 166;
                                                                                                                                                                                                                                                                     293 IDTNGAGDAFVGGFLSQLVSDKPLTECIRAGHYAASIIIRRTG 335
                                                                                                                                                                                                                                            257 YDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLG 299
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                                                                                                                                                                                                 SKRORIVIFTOGRDDTI ----MATESEVTAFAVLDODO---
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3900, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 17.6%;
Matches 70; Conservative 53
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US-09-134-001C-3900
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

November 24, 2002, 23:15:54; Search time 31 Seconds (without alignments) 240.985 Million cell updates/sec Run on:

US-09-912-020-325 2393 1 MKVTLPEFERAGVMVVGDVM.......FEDGCSTTNIIKKIOQDKKG 477 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 100480 seqs, 15661496 residues Searched:

100480

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result	6	Query	1	9	í	
	score	March	watch Length DB	<u> </u>	ID	Description
1	2393	100.0	477	10	US-09-741-669-469	Sequence 469, App
7	2393	100.0	477	10	US-09-912-020-325	Sequence 325, App
e	2393	100.0	477	10	US-09-815-242-10301	10301
4	2265	94.7	477	10	US-09-815-242-13759	П
2	1350.5	56.4	474	10	US-09-815-242-12079	Sequence 12079, A
9	197	8.2	308	10	US-09-815-242-11854	Sequence 11854, A
7	191.5	8.0	305	10	US-09-815-242-10892	Sequence 10892, A
œ	178	7.4	306	10	US-09-815-242-11035	
σ	169	7.1	309	10	US-09-741-669-479	4
10	169	7.1	309	10	US-09-815-242-10406	
11	167	7.0	310	10	US-09-815-242-13976	Sequence 13976, A
12	165	6.9	309	10	US-09-815-242-13883	٠.
13	158	9.9	309	10	US-09-815-242-10180	Sequence 10180, A
14	145	6.1	132	10	US-09-815-242-5399	Sequence 5399, Ap
15	145	6.1	132	10	US-09-815-242-12303	Sequence 12303, A
16	145	6.1	132	10	US-09-815-242-12875	Sequence 12875, A
17	145	6.1	132	10	US-09-815-242-13151	Sequence 13151, A
18	139.5	5.8	304	10	US-09-815-242-13017	Sequence 13017, A
19	139.5	5.8	304	10	US-09-815-242-13153	Sequence 13153, A

Sequence 5192, Ap Sequence 11024, A Sequence 10513, A Sequence 262, App Sequence 10376, A	Sequence 13340, A Sequence 1334, A Sequence 33, Appl Sequence 33, Appl Sequence 6, Appli Sequence 6, A	Sequence 113, Appl Sequence 113, Appl Sequence 11396, A Sequence 36, Appl Sequence 11497, A Sequence 6, Appl Sequence 10775, A	Sequence 6, Appli Sequence 2, Appli Sequence 4, Appli Sequence 6, Appli Sequence 18, Appli Sequence 18, Appli Sequence 11133, A
0 US-09-815-242-5192 0 US-09-815-242-11024 0 US-09-815-242-10513 0 US-09-815-242-10376 0 US-09-815-242-10376	10 US-09-815-21340 10 US-09-815-242-11340 9 US-09-861-289-33 10 US-09-861-289-33 10 US-09-861-289-30	12 US-U9-29-1 12 US-U9-971-536-64 9 US-09-971-536-64 10 US-09-815-242-11396 9 US-10-047-260-36 10 US-09-815-242-11497 10 US-09-815-242-1175 10 US-09-815-242-1175	0 US-10-075-460-6 0 US-09-887-052-2 0 US-09-887-052-4 0 US-09-887-052-6 0 US-09-934-901-18 0 US-09-914-868-8 0 US-09-815-242-11133
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ALIGNMENTS

RESI US-1	RESULT 1 US-09-741-	RESULT 1 US-09-741-669-469
Š	equence	Sequence 469, Application US/09741669
ã č	atent A	Patent No. US20020022718A1
5	APPLICANT.	GENERAL INFORMATION: ADDITONT FORESTH P Allen
	APPLICANT	Ohlsen,
	APPLICANT:	, Judith W.
	TITLE C	Genes identified as
	TITLE C	TITLE OF INVENTION: proliferation of E. COLI ETER PREPERENCE: PLITER ONGR
	CURRENT	CURRENT APPLICATION NUMBER: US/09/741,669
	CURRENT	CURRENT FILLING DATE: 2000-12-19
-	PRIOR #	PRIOR APPLICATION NUMBER: US 60/173005
	PRIOR	PRIOR FILING DATE: 1999-12-23
	NUMBER OF	NOMBER OF SEQ ID NOS: 481 CORTWINDE: PastSEO for Windows Varsion 4 A
໌ ທ	SEC ID NO 469	10 469
	LENGTH: 477	1: 477
	TYPE: PRT	
; US-(ORGANISM: 09-741-669	; OKGANISM: ESCRETIONIA COLI US-09-741-669-469
ŌÀ	Query Match	Query Match 100.0%; Score 2393; DB 10; Length 477; Bast Loral cinilarity 100.0%; Dred No. 3.7c.191.
Ě	Matches	vative 0;
δχ	1	MKVTLPEFERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNI 60
Op	1	MKVTLPEFERAGYMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNT1EERPGGAANVAMNI 60
δý	61	ASLGANARLYGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLD 120
Dp	61	ASLGANARLYGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLD 120
٥y	121	FEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQOMIQLARKAGVPVLIDPKG 180
Op	121	FEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKG 180
οy	181	TDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLL 240
QQ	181	TOFERYRGATLITPULSEFEAVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLL 240

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              ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL 420
                                                                                                                                                    ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL 420
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                                                          STVSPIELENAVRGRADTGFGVMTEEELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             REQUIRED FOR PROLIFERATION IN
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                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Oblisen, Kari L.
APPLICANT: Trawick, John
APPLICANT: Frosyth, R. Allyn
APPLICANT: Frosyth, R. Allyn
APPLICANT: Frosich, Jamie M.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: ESCHERICHIA COLI
FILE REFERENCE: ELITRA.001DV1
FILE REPERENCE: ELITRA.001DV1
FILE REPERENCE: 2001-07-23
PRIOR FILLING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 09/492, 709
PRIOR FILLING DATE: 1999-01-27
PRIOR FILLING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 485
SOFTWARE: FASTEED for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                         Sequence 325, Application US/09912020 Patent No. US20020045592A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 477; Conservative
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US-09-912-020-325
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121 FEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKG 180
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: PROKARYOVES

FILE REPERENCE: ELITRA.011A
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/2019, 848
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PRIOR PRIOR DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-110-23
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Pred. No. 3.7e-191;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10301
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10301, Application US/09815242
Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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100.0%;
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Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Escherichia coli
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Matches 477; Conservative
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361 ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL 420
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  241 QPNKAPLHM?TQAQEVYDVTGAGDTVIGVLAATLAAGNTLEEACYFANAAAGVVVGKLGT
                                                                                                                                                     STVSPIELENAVRGRADTGFGVMTEEELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-05-37
PRIOR FILING DATE: 2000-05-37
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/255,931
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-02-02
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FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12079, Application US/09815242 Patent No. US20020061569A1
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Haselbeck, Robert
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-815-242-12079
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APPLICANT: W
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                                                                                      61 ASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 TDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLL 240
                                                               STVSPIELENAVRGRADTGFGVMTEEELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL 360
                                                                                                                                                   361 ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL 420
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tammoto, Robert T.
APPLICANT: Xu. H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/25/93
PRIOR APPLICATION NUMBER: 60/25/931
PRIOR APPLICATION NUMBER: 60/25/931
PRIOR APPLICATION NUMBER: 60/25/931
PRIOR APPLICATION NUMBER: 60/25/931
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-20-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASSESEQ FOR WINDOWS VERSION 4.0
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13759, Application US/09815242 Patent No. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10892, Application US/09815242 Patent No. US/0020601569Al GENERAL INFORMATION: APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
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; ORGANISM: Enterococcus faecalis
US-09-815-242-10892
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APPLICANT:
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299
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                                                                                                                                              QPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGT 300
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                                                                                                                                                                                                                                                                                            TDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLL
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APPLICANT: ASSKING, Judith W.
APPLICANT: Syskind, Judith W.
APPLICANT: APRLICANT: Asalib.
APPLICANT: Wall, Daniel
APPLICANT: Tawaick, John D.
APPLICANT: Tawaick, John D.
APPLICANT: Tamanoto, Robert T.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Suncerial Genes in
TITLE OF INVENTION: Prockaryotes
FILE REFERENCE: ELITRA.011A
CURRENT PRILOTATION NUMBER: G0/206,848
PRIOR APPLICATION NUMBER: G0/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: G0/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: G0/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: G0/253,625
PRIOR APPLICATION NUMBER: G0/253,938
PRIOR APPLICATION NUMBER: G0/253,938
PRIOR APPLICATION NUMBER: G0/269,308
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Pred. No. 4.7e-09;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11854, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-09-815-242-11854
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Best Local 9
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EGFEGVDPQPL--HERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDP-- 178
                                                 113 GGNGHLSPAVLARHEHLLEQ-----AQVVVCQLESPLETVGHVLRRAHALGKTVILNPAP 167
                                                                                                                     233
                                                                                                                                                                             224
                                                                                                                                                                                                                                        EQGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGV 293
                                                                                                                                                                                                                                                                             13 VMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGG----AANVAMNIASLGANARL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 --KGTDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVE---RGMKLIADYELSALLVTRS
                                                                                                                                                       70 VGLTGIDDAARALSKSLA--DVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLD----
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: PROKARYOLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
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Best Local Similarity 22.8%; Pred. No. 1.3e-08;
Matches 72; Conservative 63; Mismatches 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TILLE OF INVENTION: PIGALTYCES
FILE REFERENCE: ELITER, 0.11A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,846
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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DB 10;
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Pred. No. 1e-06;
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Patent No. US20020061569Al
GENERAL INFORMATICN:
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
Xu, H. Howard
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Best Local Similarity 24.5%;
Matches 77; Conservative 47
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US-09-741-669-479
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283 AIAVTRKGAÇPSVP 296
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SOFTWARE: FastSEQ for
SEQ ID NO 479
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US-09-815-242-10406
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QGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAG-NSLEEACFFANAAAGV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 APALEQVPEELLNVTDMIVPNETETEILTGIKITDEASMRKAAEALHQLGIEAVIITVGS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 GGAANVAMNIASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVL 110
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                                                                                                           ----KGTDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSE 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKGANQAVAAARLGAKVAFISCIGSDSIGKTMKNAFAQEGID-----TTH-----IN 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CART, OTHER, OTHER, APPLICANT: CART, OTHER, OTHER, APPLICANT: Yangmoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-27
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11035, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION: APPLICANT: Haselbeck, Robert
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
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LENGTH: 306
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Best Local S
Matches 66
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67 ARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFEEGFE 126
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259 VTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGTSTVSPIELE 309
                               248 TTAAGDTFNGGFVTALLEEKSFDEAIRFGQAAAAISVTKKGAQSSIFTRQE 298
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                                                                                                                                                                                             Sequence 479, Application US/09741669
Patent No. US20020022718A1
GENERAL INFORMATION:
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Syskind, Judith W.
TITLE OF INVENTION: Genes Identified as required for TITLE OF INVENTION: proliferation of E. coli FILE REFERENCE: ELITRA.009A
CURRENT APPLICATION NUMBER: US/09/741,669
CURRENT FILING DATE: 1999-12-19
PRIOR APPLICATION NUMBER: US 60/173005
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PRIOR APPLICATION NUMBER: 66/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PASSES OF WINDOWS VERSION 4.0
SED ID NO 13376
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Zyskind, Judith W.
Wall, Daniel
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APPLICANT: Haselbeck, Robert
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TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/255,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/255,931
PRIOR APPLICATION NUMBER: 60/255,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/250,9308
PRIOR PRICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
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FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
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SOFTWARE: FastSEQ for Windows Version 4.0
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
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Yamamoto, Robert T.
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Matches 77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 GVVVGKLGTSTVSP 305
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283 AIAVTRKGAQPSVP 296
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                28 PTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANARLV----GLTGIDDAARALS 83
                                                                                                                                                                                                                      24 PEGKLRCSAPV-----FEPGGGGINVARAIAHLGGTATAIFPAGGATG----EHLV 70
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       Length 310;
                                                                             Indels
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APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                          36; Mismatches 115;
Query Match 7.0%; Score 167; DB 10; Best Local Similarity 27.1%; Pred. No. 1.5e-06; Matches 85; Conservative 36; Mismatches 115;
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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16;

14;

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79 ARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFE---EGFEGVDP----- 130
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TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/240,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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Best Local Similarity 25.4%; Pred. No. 8.2e-06;
Matches 80; Conservative 37; Mismatches 122;
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10180
LENGTH: 309
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APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
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Zyskind, Judith W.
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US-09-815-242-10180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 KGESTGVALIFVNG-EGENVIGIHAGANAALSP--ALVDAQRERIAQADALLMQLESPLE 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVQQMIQLARKAGVPVLIDP --- KGTDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVER 215
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APPLICANT: 2yskind, Judith W.
APPLICANT: 4011. Daniel
APPLICANT: Tranick, John D.
APPLICANT: Tranick, John D.
APPLICANT: Tanamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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Best Local Similarity 24.8%; Pred. No. 2.2e-06;
Matches 67; Conservative 39; Mismatches 134;
                         PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SCATUANG DATE: 309
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PRIOR PAPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PELICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
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APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Salmonella typhi
Uṣ-09-815-242-13883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 ESIRYVDLVIPEKGWGQKEDDVEKFDV----DVFVMGHDWE-----GEFDFLKDKCEVIY 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
                                                                                                                                                                                                                            6.1%; Score 145; DB 10; Length 132; illarity 31.7%; Pred. No. 2.9e-05; Conservative 29; Mismatches 48; Indels 2
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APPLICANT: 478XING, JUGILIN W.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamancto, Robert T.
APPLICANT: Xu H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: 10401401A
CURRENT PELLING BATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/255,931
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-02-26
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-02-26
PRIOR PILING DATE: 2000-02-26
PRIOR PILING DATE: 2000-02-26
PRIOR PILING DATE: 2000-02-26
PRIOR PILING DATE: 2000-01-2-22
PRIOR PILING DATE: 2000-02-26
PRIOR PILING DATE: 2000-01-2-22
PRIOR PILING DATE: 2000-01-2-22
PRIOR PILING DATE: 2000-01-2-22
PRIOR PILING DATE: 2000-01-2-22
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5399
LENGTH: 132
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SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US20020061569A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT CRGANISM: Staphylococcus aureus US-09-815-242-12303
                                                                                                                                 ; ORGANISM: Staphylococcus aureus US-09-815-242-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-815-242-12303
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E. coli proliferat Escherichia coli p E. coli DNA for ce Salmonella typhi D Haemophilus influe

Description

SUMMARIES

Haemophilus influe

Pseudomonas aerugi

DNA sequence upstroligonuclectide fo Oligonuclectide fo N. meningittidis par Neisseria meningit Nuclectide fo Oligonuclectide f

Haemophilus influe DNA encoding novel

Sscherichia coli p

WO200044906-A2 03-AUG-2000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Human ORF2164

Pyrococcus abyssi Enterococcus faeca

Enterococcus faeca

Bacillus lichenifo Bacillus lichenifo Haemophilus influe

Enterococcus

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Escherichia coli; E. coli; proliferation; inhibition; screening; antimicrobial; bacterial growth; antisense therapy; antibacterial; ds.
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-US-KQD02_1/USFTO_spool/US09912020/runat_25112002_091428_24237/app_query.fasta_1.647
-DB=N_Geneseq_101002 -QFNT-fastap -SUFFTX-p2n.rng -MINMATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-blts -START-1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-ECT -THR_MAX-100 -THR_NH-0 -ALIGN-15
-WODE-LOCAL -OUTFNT-pto -NORM-ext -HEAPSTIZE-500 -MINLEN-0 -MAXLEN-200000000
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-NO_XNEXY -NO_MAMP -LARGEQUERY -NCG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPORT-7
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LeuSerSerIleGlyAlaLeuValLeuSerAspTyrAlaLysGlyAlaLeuAlaSerVal

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AAA65809 to AAA65889 and AAA66058 to AAA66138 represent nucleotide sequences derived from Escherichia coli which inhibit E. coli proliferation. AAA65890 to AAA66055 and AAB15886 to AAB16040 represent nucleotide and protein sequences associated with E. coli proliferation. AAA66056 and AAA66057 represent primers used for sequencing E. coli proliferation inhibiting nucleotide inserts in an example from the present invention. Methods from the present invention. Methods from the present invention and be used to identify a proliferation-required gene in a microorganism, by contacting a microorganism with a proliferation-required gene activity inhibitory nucleic acid identified in another organism, and determining if inhibition occurs in the second microorganism. The nucleic acid sequences identified as being required for bacterial growth and proliferation, can
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W.
                                                                                               Froelich
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Yamamoto RT,
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                      181 ThrAspPheGluArgTyrArgGlyAlaThrLeuLeuThrProAsnLeuSerGluPheGlu
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                161 GlnGlnMetIleGlnLeuAlaArgLysAlaGlyValProValLeuIleAspProLysGly
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sequence (1) consisting essentially of one of the 93 nucleotide sequences
given in AAH81202 to AAH81294, where expression of the nucleic acid in a
microorganism is capable of inhibiting proliferation of a microorganism.

(I) have antibacterial and antibiotic activities, and can be used in
c (I) have antibacterial and antibiotic activities, and can be used in
c (I) have antibacterial and antibiotic activities in thibits proliferation
of the microorganism, and the manufactured antibiotic is useful for
c reducing the activity or level of a gene product required for
proliferation of a microorganism in a subject, specifically humans. The
nucleic acids that inhibit bacterial growth or proliferation can be used
as antisense therapeutics for killing bacteria. In addition to
therapeutic applications, the nucleic acid sequences complementary to
sequences required for proliferation can be used as diagnostic tools.
For example, nucleic acid probes complementary to proliferation-required
sequences that are specific for particular species of microorganisms can
be used as probes to identify particular microorganism species in
proteins given in AAG98239 to AAH81437 encode the Escherichia coli
proteins given in AAG98239 to AAH81437 encode the Escherichia coli
proteins given in AAG98239 to AAH81488 to AAH81491
represent oligonucleotides, which are used in the exemplification of the
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                                                     Escherichia coli; identification; proliferation; microorganism; antimicrobial; antibacterial; antibiotic; gene therapy; diagnosi bacterial growth inhibition; ds.
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                                                                                                                                                                                                                                                                                                                      Novel nucleic acids encoding proteins re
proliferation, useful for screening for
                                                                                                                                                                                                                                                                                                                                                            Example 4; Page 415-417; 596pp; English
                                    protein encoding
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          (first entry)
                                                                                                                                                                                                                                                         Ohlsen KL,
                                                                                                                                                                                                                                  (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                 WPI; 2001-457376/49.
P-PSDB; AAG98421.
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Best Local Similarity:
                                 Escherichia coli
                                                                                                           Escherichia coli.
                                                                                                                                  WO200148209-A2
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           21-SEP-2001
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                         PheGluGluGlyPheGluGlyValAspProGlnProLeuHisGluArgIleAsnGlnAla
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GTTAAAGTGAATACCATCGAAGAAGGTCCGGGCGGCGGCGCGTAACGTGGCGATGATC
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Sequence 1434 BP; 328 A; 352 C; 447 G; 307
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Sesential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part
1201 GGGGCACTGGAAGCGGTCGACTGGGTAGTGTCGTTTGAAGAGGACACGCCGCAGCGCTTG 1260
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                                                              1321 GCCGGGGGTAAAGAAGTCTGGCCAACGGTGGCGAAGTGTTGTTGTTGTTGAAGACTTTGAAGAC
                                     421 IlealaGlyIleLeuProAspLeuLeuValLysGlyGlyAspTyrLysProGluGluIle
                                                                                                                    441 AlaGlySerLysGluValTrpAlaAsnGlyGlyGluValLeuValLeuAsnPheGluAsp
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antibiotic; antibacterial; drug design.
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26-MAY-2000; 20000S-207727P.
23-OCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-253625P.
22-DEC-2000; 2000US-253635P.
16-FEB-2001; 2001US-269308P.
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Xu HH;
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Yamamoto RT,
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         Matches:
Conservative:
Mismatches:
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Best Local Similarity:
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9-PSDB; AAU38165
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                                                         LysValValMetThrAsnGlyValPheAspIleLeuHisAlaGlyHisValSerTyrLeu
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27-NOV-2000;
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, thair use in the discovery of novel antibiotics, the essential genes than the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella con penumoniae, Pseudomonas aeruginosa and Enterococcus facefuls. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to invention is also useful for the identification of express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery comportainmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

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  of.
New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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                                                                         Seq ID No 9661; 511pp; English.
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GGCGCGCTGGACTGGACTGGGTTGTCTTTTTGAAGAGGATACGCCGCAACGACTG
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| GCGGTTGCGGGGAAATGTAAAAGCGAAGAAGACGAACGTTGATGAACGCGGCATGAAGCTCATT
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CAGACTATGATTTCCCTAGCGCGCCCAGGCGGCGTGCCGGTGCTCATCGATCCGAAAGGA
                                                                                                                    GlyAlaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeu
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                                                                           GlnProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspValThr
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Genome; bacterium; Haemophilus influenzae; computer readable medium;

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DD 1596552 GAATTTAAGCAAGCAAAGTACTCGTATTAGGCGACGTGATGCTTGATCGTTATTGGTTC 1596493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the complete genome sequence of the bacterium Haemophilus influenzae strain Rd. The invention relates to a computer readable medium (CRM) having recorded upon it the complete H.influenzae nucleotide sequence (I), a representative fragment of (I) or a nucleotide sequence at least 99% identical to (I). By providing the full-length genomic sequence in a computer readable form, it is possible to identify commercially important nucleic acid fragments and expression modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fragments (EMFs) of the Haemophilus genome. The EMFs can be used to regulate the expression of a nucleic acid molecule. Vectors and altered organisms comprising the predicted OMFS can be used to produce any of the polypeptide fragments of the influenzae Rd genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1830121 BP; 567399 A; 350615 C; 347389 G; 564036 T; 682 other;
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                                                                                                                                                                                                                                                                                                                                                                          Haemophilus influenzae Rd genome recorded on computer readable medium – useful for identifying commercially important nucleic acid fragments by homology searching
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 vector;
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                 organism; open reading frame;
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 expression modulating
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Best Local Similarity:
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21-APR-1995;
07-JUN-1995;
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Db 1595172 GTGATTGAAAAATTAAA 1595155
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Db 1596192 AATGTAGATTGCAAGGATTTATTAGCGAAGTTAGAAAGTGCGGTGAAAATTACGGTGCT 1596133
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                                                                                                                                                                                                                                                                          207 LysThrGluGluGluIleValGluArgGlyMetLysLeuJleAlaAspTyrGluLeuSer 226
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                                          GlyvalAspProGlnProLeuHisGluArgIleAsnGlnAlaLeuSerSerIleGlyAla 146
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                                                                                                147 LeuValLeuSerAspTyrAlaLysGlyAlaLeuAlaSerValGlnGlnMetIleGlnLeu 166
                                                                                                                                                                                                                    ArgGlyAlaThrLeuLeuThrProAsnLeuSerGluPheGluAlaValValGlyLysCys 206
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prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential companies, the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella cole sendomonas aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antiSense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
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                                                                                                                                                                                                           Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
                                                                                                                                                            Pseudomonas aeruginosa DNA for cellular proliferation
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Xu HH;
BP.
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Query Match:
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27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
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26-MAY-2000;
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                     US-09-912-020-325 (1-477) x AAS54344 (1-1425)
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The invention relates to a genetically-engineered outer membrane vesicle (bleb) preparation from a Gram-negative bacterium for use as a vaccine. The blebs of the invention are improved with respect to their immunogenicity and toxicity by the introduction of one or more genetic changes to the chromosome of the bacterium from which the blebs are derived. The changes made include the upregulation of protective antigen expression, the downregulation of immunodominant non-protective antigen expression, and genetic changes which result in detoxification of the Lipid A moiety of lipopolysaccharide (LPS). The invention also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified Gram-negative bacterium; outer membrane vesicle; bleb; vaccine; genetically modified; protective antigen expression; LPS detoxification; LPS; lipid A; homologous recombination vector; immunisation; immunoprotective; non-toxic; paediatric; ds.
                                                                                                                                                                                                          1138 ACTCGCCTGAAGGGCGTTGGCCGGCCGATCAACTCGGTGGACCGGCGCATGGCGGTACTC 1197
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AlaAsnAlaArgLysLeuGlyAspArgLeuIlevalAlaValAsnSerAspAlaSerThr
                                                                    GAACAGGCGCGCCCCAGGGCGACCGCCTGATCGTCGGGGGTCAACGACGACGCCTCGGTC
                                                                                                                                             LysArgLeuLysGlyAspSerArgProValAsnProLeuGluGlnArgMetIleValLeu
                                                                                                                                                                                                                                                                                   GlyAlaLeuGluAlaValAspTrpValValSerPheGluGluAspThrProGlnArgLeu
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Thonnard J,
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preparations are made, a vector suitable for performing recombination

sevents (for the generation of the modified bacterial strains),

bacterially-derived nucleic acid sequences used in such a vector, and an immunoprotective and non-toxic Gram-negative bleb, ghost, or killed whole call vaccine suitable for paediatric use. The bleb preparation is useful in the manufacture of a mediament for immunishing a human host against a disease caused by infection of one or more of the following: Neisseria meningitidis, Neisseria gonorrhoeae, Haemophilus influenza, Moraxella cataritalis, Pseudomonas aeruquinosa, Chlamydia trachomatis, and Chlamydia catarithalis, Pseudomonas aeruquinosa, Chlamydia trachomatis, and Chlamydia trachomatis. The invention may also be used to provide immunisation against the influenza virus. Bacterially derived nucleotide sequences of the influenza virus acterially derived nucleotide sequences of the invention are used in the performance of homologous recombination events up to 1000 bp upstream of a bacterial chromosomal gene in order to either con-toxic Gram-negative bleb, ghost, or killed whole cell vaccines are more immunogenic, less toxic and safer, and are particularly useful for paediatric use. The present sequence represents a specifically con-toxic maned Haemophilus influenzae nucleic acid sequence.
       strains from which the bleb
   Gram-negative bacterial
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Sequence 1001 BP; 301 A; 225 C; 168 G; 307 T; 0 other;

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The invention relates to an immunogenic composition comprising an antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as.
                                                                                                         Upstream sequence; ds; Antibacterial; vaccine; bleb;
Gram-negative bacteria; outer membrane; LPS; lipopolysaccharide;
meningitis; bacteraemia; otitis media; pneumonia; chronic bronchitis;
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                                                                                                                                                                                            New immunogenic composition comprising an antigen derived from a pathogen and a bleb preparation from Neisseria meningitidis, useful a vaccine for treating or preventing disease caused by the pathogen
AlaLeuLeuValThrArgSerGluGlnGlyMetSerLeuLeuGlnProGlyLysAlaPro
                                                              267 IleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhePhe
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P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA sequence upstream of htrB #3 gene.
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ID ABK37818 standard; DNA; 1001 BP.
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08-FEB-2001; 2001GB-0003170.
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106 ATTAGTGTATTAGCAACCACTTAGCAGATGGACGTTCTTTCGAAGAATCTTGTTACCTA 47

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from a non-typeable H. influenzae is useful as an adjuvant in an immunogenic composition comprising one or more pneumococcal capsular polysaccharides or protein antigens. The present sequence is an upstream sequence from an N. meningtidis, H.influenzae or M. catarrhalis gene involved in LPS biosynthesis, which either up regulates or down
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Mismatches:
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Matches:
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated C, to uracil, then part of the genomic CC The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue cypes and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously.

ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the the allows the invarience of processive of cytosine methylation described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide for detecting cytosine methylation SEQ ID NO 7681.
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Conservative:
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05-SEP-2000; 2000DE-1044543.
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                                                                                                                                                                                                                                                                                                                                                                                                               GluGluIleAlaGlySerLysGluValTrpAlaAsnGlyGluValLeuValLeuAsn 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                       ArgGlyGluLysValValMetThrAsnGlyValPheAspIleLeuHisAlaGlyHisVal
                                                                                                                                                                                                                                                                                                                                                                                                                       SerLeuLeuGlnProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyr
                                                                                  AsnSerLeuGluGluAlaCysPhePheAlaAsnAlaAlaAlaGlyValValValGlyLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide for detecting cytosine methylation SEQ ID NO 7682
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is 'treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic cample of DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymer phisms (SNP's); and (11) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many c residues to be determined simultaneously. Appliation described in the disclosure of the invention.
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856.00
79.91%
78.63%
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05-SEP-2000; 2000DE-1044543
01-SEP-2001; 2001WO-EP10074
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                                                                              (EPIG-) EPIGENOMICS
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ThrGlyPheGlyValMetThrGluGluGluLeuLysLeuAlaValAlaAlaAlaAlaALys 337

ArgGlyGluLysValValMetThrAsnGlyValPheAspIleLeuHisAlaGlyHisVal 357

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Scarlato V;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes methods of obtaining immunogenic proteins from Nelsseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Nelsseria meningitidis genomic DNA sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Nelsseria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81321 represent PCR primers used in the isolation of Nelsseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent Nelsseria meningitidis MenB polynucleotide ORF sequences, which are all used in the exemplification of the present
                                                                                                                                                                                IleValLeuGlyAlaLeuGluAlaValAspTrpValValSerPheGluGluAspThrPro 417
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                          SerTyrLeuAlaAsnAlaArgLysLeuGlyAspArgLeuIleValAlaValAsnSerAsp
                                                                                                                                                                                                                                226 ATTGTGTTGGGCGTATTGGAAGCGGTCGATTGGGTAGTGTCGTTTGAAGAGATACGTCG
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                                                                                        378 AlaSerThrLysArgLeuLysGlyAspSerArgProValAsnProLeuGluGlnArgMet
                                                                                                                                                                                                                                                                                                                                                                      GluGluIleAlaGlySerLysGluValTrpAlaAsnGlyGlyGluValLeuValLeuAsn
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Ratti G, So
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AAA81463 standard; DNA; 78845
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composition can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to C Neisserial bacteria. For example, some of the identification due to C Neisserial bacteria. For example, some of the identification of sequences addor against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious computationally organism-specific probes. Attempts to make efficacious will william also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious confined mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than
  and antibodies
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46505 GGGCTGTTGTCCGTAACCGCCACGACGACGCGCTCGATGCTG
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                                                                                                                                                                                                                                                                                                                                             Sequence 78845 BP; 19372 A; 21111 C; 19042 G; 19318 T; 2 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                           <u>.,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine; diagnosis; antigen; detection; infection; gene therapy; antibacterial;
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Rappuoli R
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                                                                                                                                                                  GCCGGAATGGGTTTGGCGGCAGGCTGCACCATGCCCGAAGCCATGTACCTTGCC
LeuLeuValThrArgSerGluGlnGlyMetSerLeuLeuGlnProGlyLysAlaProLeu
                                                            GTTTTACTGACCCGAAGCGAAGAGCATGACCTTGTTCAGCGAAGGCGAA---CCGATT
                                                                                                                                HisMetProThrGlnAlaGlnGluValTyrAspValThrGlyAlaGlyAspThrValIle
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Scarlato V,
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Ratti G, Scarselli M,
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08-OCT-1999; 99WO-US23573.
28-FEB-2000; 2000GB-0004695.
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Galeotti C, Mora M,
Frazer CM, Grandi G;
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due to Neisserial bacteria or as a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised to Neisserial bacteria. Computers, computer memory, computer storage medium or computer databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the outer membrane proteins currently
preventing infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 ThrGluGluGluIleValGluArgGlyMetLysLeuIleAlaAsplyrGluLeuSerAla
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                                                                                                                                                                              Sequence 349980 BP; 82523 A; 82940 C; 96712 G; 87805 T; 0 other;
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49
100
used in compositions for treating
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Mismatches:
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Matches:
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                                                                      307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptide encoded by operon including virulence genes of Neisseria meningitidis, useful as vaccine component for treating or preventing meningitis and for identifying antimicrobial drug
                        248662 GCCGGAATGGGCTTGGGTTTGGCGGCAGGCTGCACCATGCCCGAAGCCATGTACCTTGCC
                                                                                         248722 AATACTGCGGCGCGGGGTTGTCGTGGCGAAACTCGGTACGCCGGAA
268 GlyvalLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhePheAla
                                                                      AsnAlaAlaAlaGlyValValValGlyLysLeuGlyThrSerThrValSerProIleGlu
                                                                                                                                                                                                                                                                                                                                                                                                  Meningitis; virulence; gene; antibacterial; vaccine; veterinary; infection; Gram-negative bacteria; antimicrobial; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virulence genes and related PCR primers of the invention.
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                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis virulence gene #26
                                                                                                                                                                               Db 248782 TIGATCAAGGCATIGICAGGGCAAICA 248808
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                                                                                                                                           LeuGluAsnAlaValArgGlyArgAla 316
                                                                                                                                                                                                                                                        BP.
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P-PSDB; AAU72936.
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969 156 49 103

Length: Matches: Conservative: Mismatches:

1.74e-59 745.50 66.34% 50.49% 31.15%

Best Local Similarity:

Query Match:

Percent Similarity

Alignment Scores:

Pred. No.:

Score:

Indels:

US-09-912-020-325 (1-477) x AAS97221 (1-969)

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669
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                                                                               00 GATGTGTCCCGTATTTCGCCCGAAGCCCCCGTGCCGAAAATCGGACAAATCGAC 159
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              40 TTCGCGCAAGCCAAAGTCCTGGTTGTCGGCGACGTGATGCTCGACTGTATTGGTTCGGC
                                                            28 ProThrSerArgIleSerProGluAlaProValProValValLysValAsnThrIleGlu
                                                                                                                        48 GluArgProGlyGlyAlaAlaAsnValAlaMetAsnIleAlaSerLeuGlyAlaAsnAla
                                                                                                                                                                                                                                                                                                                                                                        128 ValAspProGlnProLeuHisGluArgIleAsnGlnAlaLeuSerSerIleGlyAlaLeu
PheGluArgAlaGlyValMetValValGlyAspValMetLeuAspArgTyrTrpTyrGly
                                                                                                                                                  160 CAACGCGGGGGGGGGGGAAATGTCGCGGCAAATGTCGCTTCGCTTCGCTGGGCGCCAAAGTA
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Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              related
or prevent H. pylori
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given
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                                                                                                                                             Key
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The present sequence encodes a Helicobacter pylori cytoplasmic protein. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic contigs generated by mechanically shearing the bacterial DNa. The sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNa. The sequences were analysed for ORF of at least 180 nuclectides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coll hosts. GGGGTAGTGGGAGATGATTTAAAAGGCAAGCATTTCATTAGCACTTTAAATTCTATAAGG 126 ValLysCysAspPheValSerVal---ProThrHisProThrIleThrLysLeuArgVal 109 90 GlyGlyAlaAlaAsnValAlaMetAsnIleAlaSerLeuGlyAlaAsnAlaArgLeuVal 71 GlyLeuThrGlyIleAspAspAlaAlaArgAlaLeuSerLysSerLeuAlaAspValAsn Sequence 1272 BP; 412 A; 232 C; 284 G; 344 T; 0 other; 1272 177 77 154 25 Length:
Matches:
Conservative:
Mismatches:
Indels: (1-1272)Gaps: US-09-912-020-325 (1-477) x AAT68016 734.50 58.66% 40.88% 30.69% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match: 7 29 Score:

ATTGACACTICAGGTGTTTTAATAGATAAACCCGTTGCACCACGCTTAAAACGCGCATC 186

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994 AAAAGGCTTAAGGGGGATAAACGCCCCATAGTGAGGGGAAAAAGACAGGGGGGTTTCTTTTA 1053
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277 587 297 527 317 467 337

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Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA
                                                                                                                  Human: cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
drug; side effect; cancer; central nervous system; cardiovascular;
gastrointestinal; respiratory system; single nucleotide polymorphism;
SNP; cell differentiation; ds.
                                                                                                    Oligonucleotide for detecting cytosine methylation SEQ ID NO 7683.
Claim 12; 56pp + Sequence Listing; 56pp; German.
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                                              ABQ21092 standard; DNA; 707
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05-SEP-2000; 2000DE-1044543.
                                                                                                                                                                                                                         01-SEP-2001; 2001WO-EP10074
                                                                                  (first entry)
                                                                                                                                                                                                                                                                                        Piepenbrock C,
                                                                                                                                                                                                                                                                      (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                     WO200218632-A2.
                                                                                 12-JUL-2002
                                                                                                                                                                   Homo sapiens
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                                                                ABQ21092;
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-cpG-3', present in a genomic sample of DNA. The sample is treated obsenially to convert cytosine (C) but not methylated C. to tracil, then part of the genomic CDNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridisation to both classes, each with at least one member, of oligonuclectides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue methylation status of many C residues to be determined simultaneously.

ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method and contrained simultaneously. the invention the disclosure of

Search completed: November 26, 2002, 21:16:52 Job time : 1025 secs

G; 329 T; 1 other; Sequence 707 BP; 137 A; 62 C; 178

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707
133
47
55
1
      Length:
Matches:
Conservative:
Mismatches:
Indels:
      4.25e-55
696.00
76.60%
56.60%
29.08%
                    Percent Similarity:
Best Local Similarity:
Alignment Scores:
        Pred.
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JS-09-912-020-325 (1-477) x ABQ21092 (1-707)

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ACAAACTTTAACGTAATAACCGAAAAAAACTAAAACTAACCGTAACGACAACGCGTAAA 407
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              AsnSerLeuGluGluAlaCysPhePheAlaAsnAlaAlaAlaGlyValValValGlyLys
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Command line parameters:
-MODEL-frame+ p2n.model -DEV-Xlp
-MODEL-frame+ p2n.model -DEV-Xlp
-MODEL-frame+ p2n.model -DEV-Xlp
-DE-EGG 12.J/USPTO_SPOOJ/USO9912020/runat_25112002_091428_24259/app_query.fasta_1.647
-OB-/CGG 12.J/USPTO_SPOOJ/USO9912020/runat_25112002_091428_24259/app_query.fasta_1.647
-DB-EST -OFMT-fastap -SUFFIX-P2n.rst -MINMATCH-0.1 -LOOPCL=0 -LOOPEXT-0
-UNITS-b1ts -START=1 -END-1 -MATRIX-blosum62 -TRANS-human40 cd1 -LIST-45
-DOALIGN-200 -THR.SCORE-PCT -THR.MIN-100 - ALKEN-1500000000
-USER-USO9912020_GCGN_1_1_2024_Grunat_2511200_091428_24259 -NCPU-6 -ICPU-3
-NOALDEY-PCT-PCT-0 -THREADS-1 -XGAPPO-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
-YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
                                                                                                     November 26, 2002, 10:25:42; Search time 2404 Seconds (without alignments) 3213.497 Million cell updates/sec
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2393
1 MKVTLPEFERAGVMVVGDVM......FEDGCSTINIIKKIQQDKKG 477
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                        OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                          16154066 seqs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                              Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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em_gss_hum:*
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Perfect score:
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                                                                                                                                                                                                                           sequence:
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em_gss_mus:* em_gss_other:

em_gss_pro:* em_gss_rod:*

em_gss_mam:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			dР			SUMMARIES			
Result No.	ult No. Sc	ore	uery		DB	ID	10		
•		290	12.1	505	10	BE332786	BE332786 us		
	7	233	6.7	483	17	BH404405	BH404405 AC	-	
υ	٣	220		550	17	вн390803	вн390803 А	G-ND-140	
		Н		502	13	BM167110	BM167110 E	~	
	_	8.5	7.5	555	13	BI786239	BI786239 S	ai34e10.	
		178		9	74	BQ996249	BQ996249 Q	0	
	-	7 P	٠	1031	1 5	AKU1/229 BE043547	AKO1/229 Mi		
	٦,-	, c		7.7	7.	B1343347		. 00	
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υ	-	7.5		689	13	BJ165221	BJ165221 B.	J165221	-
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	13	162		989	14	BQ995975	BQ995975 Q	GG11110.	
	4.	128		7.29		BI308004	BI308004 E	ST529414	
	13	127		603	7,5	BF64 2033	BF642033 N	FUI4AU91	
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	7.	01.	•	150	7 ;	BJ435/42	BJ435/42 B	7470011	
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	22	156		698	;;	BF154250	BF154250	57F11 Ma	
	23	156		669	3 (B.1432465	B.7432465 B.	1432465	
	24	156		705	13	BJ377283	BJ377283 B.	3377283	
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	28 15	S		268	6	AI995602	AI995602 70	1675044	
		н		649	13	BJ435218	BJ435218 B	J435218	
	30 15	4	•	603	10	AV828468	AV828468 A	V828468	
	-	♥,		792	17	BG88833	BG88833 E	ST514684	
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	-	ન (708	7 .	BG131085	BG131085 E	ST463977	
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		vς		100	7 .	BE920333	BE920333 E	205 42 430	
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	٣	6		553	10	AW219042	ы	ST30152	
	Н	6		616	13	BI639334	S	D21893	
υ		8		528	10	BE100952	5	I-R-BJ1	
						ALIGNMENTS			
RESULT	LT 1								
BE33278	2786								
LOCU	S	BE33	2786			505 bp mrna	linear EST 1	-JUL-2000	
DEFI	DEFINITION	us53d03.	d03.x1	Perkins SW.RFAF		LRH Mus musculus cDNA CIC ECOLI P76658 ADD-HEDTOST	one IMAGE:3216	101 3' RNA	
		Sedu		3M - MC		ביים מכמחים	III '' TEURINTE	CN.	
ACCE	ACCESSION	BE332786		•					
VERSION	NOI	BE33	2786.1	GI:92	20656	62			
SOUR	SOURCE	house	mons	ď					
OR	ORGANISM	Mus		13		,			
		Euka	Eukaryota; Mammalia: F	Metazoa		Chordata, Craniata, Ver Rodentia: Sciurognathi	Vertebrata; Euteleostomi hi: Muridae: Murinae: Mu	ostomi; ae: Mus	
REFE	REFERENCE	7	1 (bases 1	1 to 505)	_			i	
AU	AUTHORS	Marr	a, M., F	iillier	÷	, Kucaba, T., Martin, J.,	, Beck, C., Wylie, T	Ί.,	

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BH404405.1 GI:17350621
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Best Local Similarity:
                                                                                               Anopheles.
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Pred. No.:
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 VERSION
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="primary sorted bone marrow cells"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/note="Vector: pzL1; Site_1: Sal1; Site_2: Eag1; cDNA made
by oligo-dr priming. Library amplified by stretch PCR.
Subtraction method: Bonaldo, et al., Genome Research
6:791. Library constructed by Dr. Archibald Perkins (Yale
University)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AG-ND-140M3.TR.1 ND-TAM Anopheles gambiae genomic clone AG-ND-140M3 BH404405
 Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person
F., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter
                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1066249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         427
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                                                                                     Contact: Marra MWashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Feb: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetLysValThrLeuProGluPheGluArgAlaGlyValMetValValGlyAspValMet
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Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                       Possible reversed clone: similarity on wrong strand
Seg primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 others
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Conservative:
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                                                                                                                                                                                                                                                                                                                                              /db_xref-"taxon:10090"
/clone="IMAGE:3216101"
/clone_lib="Perkins LRH"

    .505
    /organism="Mus musculus"

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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                 /strain="BALB/c"
                                                                                                                                                                                                                                                                                                                                                                                           /sex="female"
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                                                                             Unpublished (1999
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Best Local Similarity:
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Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J. Direct Submission of BAC-end sequences from Anopheles gambiae (Unpublished (2001)) Other_GSSS: AG-ND-140M3.TF.1
                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center Oniversity, College Station, Texas 77843-2123, USA using a HindIII partial digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 SerLysSerLeuAlaAspValAsnValLysCysAspPheValSerValProThrHisPro 102
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                    Anopheles gambiae
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 ValThrLeuProGluPheGluArgAlaGlyValMetValValGlyAspValMetLeuAsp
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                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Site_1: HindIII"
131 t
                                                                                                                                                                                                                                                                             Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:7165"
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/clone_lib="ND-TAM"
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a 132 c 93 g 131
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                                                                                                                                                                                                                                                           Contact: Brendan J Loftus
African malaria mosquito.
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Class: BAC ends.
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REFERENCE AUTHORS TITLE JOURNAL

COMMENT

ACCESSION VERSION KEYWORDS SOURCE

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mena isolated using oligo(dT)-cellulose chromatography. First strand cDAA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to After packaging, the phagemid vector (pAD-GAL4) was excised from the HybrilaAP vector and plasmid DNA.
                                                                                                                                                                                                                                                               BM167110 502 bp mRNA Linear EST 04-DEC-2001
EST569633 PyBS Plasmodium yoelii yoelii cDNA clone PYCOC88 5' end,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was
collected from BALB/CByJ mice infected with Py17XL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: carlton@tigr.org
Spr clone info, please contact the Malaria Research and Reference
Reagent Resource Center, ATCC
http://www.malaria.mr4.org/mr4pages/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium joelii joelii
Bukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (Dases 1 to 502)
Carlton,J.M., Daly,T.M., Long,C.A., Bergman.L.W., Vaidya,A.B.,
Fraser,C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
                                       82 uSerLysSerLeuAlaAspValAsnValLysCysAspPheValSerValProThrHisPr 102
130 ACTTGGTGTAAAGGTTGGTCTTATTGGTGTGGTGGTGATGACGAAGCTGCCAGTACGAT 71
                                                                                 70 TGAGGAATTGCTGACAAAAACAAATTGATGCGAAGCTAAGCCAFGATCGTCGTTGGTATC 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   502
445
36
36
36
5
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Jane Cariton
Parasite Genomics Group
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:73239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="PyBS"
                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium yoelii yoelii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="PYCOC88"
                                                                                                                                                                                                                                                                                                                                                       BM167110.1 GI:17300342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="17XL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.33e-10
179.00
50.31%
27.95%
7.48%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isolated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: ADF
                                                                                                                                                                                                                                                                                                           mRNA sequence.
BM167110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                              102 oThrile 104
                                                                                                                                                                        10 GACAATT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
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                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                            BM167110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                    RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DRIGIN
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Cother_GSSS: AG-ND-140M3.TF
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
Tel: 301 838 0208
Fax: 301 838 3543
                                                                                 BH390803 11-DEC-2001 SA Linear GSS 11-DEC-2001 AG-ND-140M3.TR ND-TAM Anopheles gambiae genomic clone AG-ND-140M3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: bloftusetigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
This clone is from an A. gambiae BAC library (ND-TAM) provided by
TH: Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M Universty BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 GTGACGACCATGGAAGTAACTGAAAAGCGCTTGCTGGTTGCAGGGGATATTATGGCTGGA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ValThrLeuProGluPheGluArgAlaGlyValMetValValGlyAspValMet-LeuAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rLeuGlyAlaAsnAlaArgLeuValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLe
:!||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone= no ... /clone_lib="ND-TAM"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
150 c 105 g 147 t
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48
16
38
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Matches:
Conservative:
Mismatches:
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/strain="PEST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:7165".
/clone="AG-ND-140M3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                  African malaria mosquito.
                                                                                                                                                                      внз90803.1 GI:17336944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.49e-15
220.00
62.14%
46.60%
9.19%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: M13 Rev
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                (bases 1 to 550)
                                                                                                                                                                                                                                            Anopheles gambiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      partial digest.
                                                                                                                                DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity:
                                                                                                                                                                                                                                                                                                           Anopheles.
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                                     RESULT 3
BH390803/c
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                                                                                                      DEFINITION
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FEATURES

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/ndc="Vector: pBluescript II SK+; Site_I: ECORI; Site_2:
XhoI; The CDNA library was constructed from mRNA isolated
germinating shoots of the cultivar Killiams. The seeds
were allowed to germinate for 24 hours prior to being
cold stressed for 2 days at 4C. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. ECORI
adapters were ligated to the blunt-ended CDNA fragments
followed by XhoI digestion. The CDNA fragments were
directionally cloned into the ECORI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (GibcoBRL). This library
was constructed in the laboratory of Dr. Randy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BQ996249 GFGHJ lettuce serriola Lactuca sativa clone OGG12F01.yg.abl QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlnMetIleGlnLeuAlaArgLysAlaGlyValProValLeuIleAspProLysGlyThr 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MetLysLeulleAlaAspTyrGluLeuSerAla-----LeuLeuValThrArgSerGlu 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlnGlyMetSerLeuLeuGlnProGlyLysAlaProLeuHisMetProThr --- GlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 CAAGTCGCACAGGCTGCAAGGAATGCTGGCGTGCCAGTAGTGTTTGATGCGGGGGGGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluPheGluAlaValValGly---LysCysLysThrGluGluGlufleValGluArgGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspPhe------GluArgTyrArgGlyAlaThrLeuLeuThrProAsnLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 LeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnAlaAlaAlaGlyVal
                                                                                                                        /clone_"GENOME SYSTEMS CLONE ID: Gni-c1065-5204"
/clone_lib="Gni-c1065"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          555
24
20
67
11
5
                                                                                                                                                                      /tissue_type="germinating shoots"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTGTTCAAGTGAAGGGAGCCTCTCCTAGCATGCCT 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                   /organism="Glycine max"/db_xref="taxon:3847"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-912-020-325 (1-477) x BI786239 (1-555)
Seg primer: -40RP from Gibco
High quality sequence stop: 421.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.14e-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178.50
48.68%
35.53%
7.46%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shoemaker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
Pred. No.:
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                                                                   source
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ORIGIN
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BQ996249
                                             FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shoemaker, R., Kelm, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, P., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BI786239 555 bp mRNA linear EST 30-NOV-2001 sai34e10.yl Gm-c1065 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1065-5204 5' similar to TR:Q9SHH5 Q9SHH5 F20D23.14 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycine max
Wararyota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                               355
                                                                                                                                              HisValSerTyrLeuAlaAsnAlaArgLysLeuGlyAspArgLeuIleValAlaValAsn 375
                                                                                                                                                                          395
                                                                                                                                                                                                                                                                                                                 408
                                                                                                                                                                                                                                                                                                                                                           281
                                                                                                                                                                                                                                                                                                                                                                                                ValValSerPheGluGluAspThrProGlnArgLeuIleAlaGlyIleLeuProAspLeu 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---ProGluGluIleAlaGlySerLysGluValTrpAlaAsnGlyGlyGluValLeuVal 455
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                              SerAspAlaSerThrLysArgLeuLysGlyAspSerArgProValAsnProLeuGluGln
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                                                               ArgLysArgGlyGluLysValValMetThrAsnGlyValPheAspIleLeuHisAlaGly
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Public Soybean EST Project
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Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Kondo, H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamotc,R., Matsumoto,H., Sakaguchi,S., Ikeqami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Chara,E., Watahiki,M., Yonada,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Censes 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AK017229 1031 bp mRNA linear HTC 19-JAN-2002 Mus musculus adult male xiphoid cartilage cDNA, RIKEN full-length enriched library, clone:5230400Mll:homolog to RIBOKINASE, full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                               GlyAspSerArgProValAsnProLeuGluGlnArgMetIleValLeuGlyAlaLeuGlu 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Asp------LeuLeuValLysGlyGlyAspTyrLysProGluGluIle 440
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                                                                                                                                                                    111111 | 111:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 | 11:3 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         345 ThrAsnGlyValPheAspIleLeuHisAlaGlyHisValSerTyrLeuAlaAsnAlaArg
                                                                                                                                   365 LysLeuGlyAspArgLeuIleValAlaValAsnSerAspAlaSerThrLysArgLeuLys
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Lettuce and Sunflower ESTs from the Compositae Genome Project http://compgenomics.ucdavis.edu/
Inpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
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Tel: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig5995, see http://cgpdb.ucdavis.edu/
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form 10 different sources of RNA from a single genotype.
Sparate cDNAS were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAS were then pooled, size-fractionated
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgpdb.ucdavis.edu/
                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyda; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
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/cultiva="L.serriola"
/db_xref="taxon:4236"
/clone="QGG12F01"
/clone=lib="QG_EFGHJ lettuce serriola"
/lab_host="E.coli"
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TAG_TISSUE-flowers pre-fertilized
TAG_SEQ=GCTTGACGGG"
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   OGG12F01, mRNA sequence
                                                               BQ996249.1 GI:22430645
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/tissue_type="xiphoid cartilage"
/clone_lib="RIKEN full-length enr:ched mouse cDNA library"
dev_stage="adult"
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                                                                                                                       /note="data source:SPTR, source key:Q9H477, evidence:ISS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RTKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemonic Sciences Certer (SCC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, San-0045, Japan (E-mail:genome-reségsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3'
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/db_xref="MGD:MGI:1903857"
/db_xref="taxon:10090"
/clone="5230400M11"
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1,26e-09
173.50
48.03%
34.87%
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                                                                                                                                         Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lactuca.
                                                                                                                    Percent Similarity:
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AUTHORS
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BQ850159
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In Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: Mois are clark NIL was constructed and seed was provided by Dr. J. Specht, University of Nebraska (Shoemaker and Specht, University of Nebraska (Shoemaker and Specht, University of Nebraska (Formand Specht, University of Nebraska (Shoemaker and Sisolated from whole seedlings of I week old greenhouse grown plants. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site and a 3' anchor. EcoRI adapters were ligated to the blunt-ended CDNA fragments followed by XhoI digestion. The CDNA fragments were directionally cloned into the EcoRI.XhoI restriction site of the pBluescript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). The library was constructed in cooperation with Dr. Paul Keim's laboratory at Northern Alizona University."

124 c 153 g 159 t 2 others
                                                                                                                                                                                                                                                                                                                      B1943547 16m-c1048 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1048-153 5' similar to TR: Q9SHH5 Q9SHH5 F20D23.14 PROTEIN. ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="whole seedlings of greenhouse grown plants"
/dev_stage="1 week old"
/lab_host="DH10B"
yValLeuAlaAlaThrLeuAla-----AlaGlyAsnSerLeuGluGluAlaCysPhePh 286
                                                                                                                                       850 AGCGCTGGCCTTCTACCTGGCTTACTACCCAAATCTGTCCTTGGAAGAAATGCTCAAGAG 909
                                                                                                                                                                                   eAlaAsnAlaAlaGlyValValValValGlyLysLeuGlyThrSerThrValSerPro 305
                                                                                                                                                                                                                             910 ATCCAATTTCATCGCTGCAGTCAGTGTACAGGCCACGGGAACACAGTCCTCTTATCCA 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Glycine max"
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/db_cref="taxones:3847"
/clone="cBNOME SYSTEMS CLONE ID: Gm-c1048-153"
/clone_lib="Gm-c1048"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
B1943547
B1943547.1 GI:16279653
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                                                                                                                                                                                                                                                                                                                                           DEFINITION
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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BI943547
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E l'Obses 1 to 736)

S Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,

Lin, H., van Damme, M., Lavelle, D., Chevalier, F., Ziegle, J., Ellison

P., Koikman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,

Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Project

http://compagenomics.ucdavis.edu/

Unpublished (2002)

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Fax: 1-(530)-752-9659

Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QGBILLNO7.yg.abl QG_ABCDI lettuce salinas Lactuca sativa cDNA clone QCBILNO7, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rieseberg, L.,
egle, J., Ellison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
                                                                                                                                                                                                                                                                    GlnMetIleGlnLeuAlaArgLysAlaGlyValProValLeuIleAspProLysGlyThr 181
                                                                                                                                                                                                                                                                                                  GluPheGluAlaValValGly---LysCysLysThrGluGluGluIleValGluArgGly 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                278
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279 TTGAAATGC-------CATGAATTGGGAGTTAAGCAAGTTCTTGTGAAACTTGGGGAA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    390 AAAACAGTCGTTGATACTACTGGTGCCGGTGATACTTTTACTGCTGCTTTTTGCTGGGCC 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 AspPhe------GluArgTyrArgGlyAlaThrLeuLeuThrProAsnLeuSer 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 MetLysLeuIleAlaAspTyrGluLeuSerAla-----LeuLeuValThrArgSerGlu 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnGlyMetSerLeuLeuGlnProGlyLysAlaProLeuHisMetProThr---GlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   330 AAAGGATCTGCCCTTTTTGTAGAAGGAGAAAAACCAATTCAGCAGCCTGCCATACTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              274 LeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnAlaAlaAlaGlyVal
                                                                                                                                                                                                                                                                                                                                                                                                                                               159 GATGGGCCCCTTCCACCACAATTATTGAATTTTGTTGATATTCTGAGTCCTAATGAAACT
572
53
20
20
58
11
                                                             Conservative:
                                                                                        Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         510 TGTGTTCAAATGAAGGGAGCCTCTCCTAGCATGCCT 545
Length:
Matches:
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CAAACGAACAGAAGGAGTCTCAAGCACAGACATTGTTGGGAGGATG
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                                                                                                                                                                                                                                                                                        Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .629
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seg primer: ADF.
                                                                                                                mRNA sequence.
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Query Match:
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                                                                                 LOCUS
                                               RESULT 10
BM169900
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AUTHORS
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KEYWORDS
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                                                                                                                                                                       from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. CDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/
belongs to contig QC_CA_Contig5995, see http://cgpdb.ucdavis.edu/
for details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         340 uLysValValMetThrAsnGlyValPheAspIleLeuHisAlaGlyHisValSerTyrLe 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 ValSerProIleGluLeuGluAsnAlaValArgGlyArgAlaAspThrGlyPheGlyVal 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 ATGCGCTGCTTGGCCGGAGCTCTCCCCTCTGAGTATTGTTGGGAGGAGAAGAAGAAGAAGAGGCC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 uAlaasnAlaargLysLeuGlyAspArgLeuIleValAlaValAsnSerAspAlaSerTh 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 424 ATGCATTCTCCCTGATGGAACTGACGCATATGCCCTTGCAAAGAAGCAGGTCGATATAA 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sProGluGluIleAlaGlySerLysGluValTrpAlaAsnGlyGlyGluValLeuValLe 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323 Met-Thr-----GluGluGluLeuLysLeuAlaValAlaAlaAlaArgLysArgGlyGl
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GAGTGCTGTGAAATGGGTAGATGAAGTCATTCCAGATGCACCATATGCCATAACTGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 GTTTCTAGCGACATGGTTGATCGGAGGTTTGGTGGCAGGGCT---ATCGGTTATGGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------PheGluGluAspThrProGlnArgLeuIleAlaGly-----
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                                                                                                         /db_xref="taxon:4236"
/clone="QGB11N07"
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                                                                                                                                                                                                                                                                                                                                                                                                                             736
62
27
29
48
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
MatcHes:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                  TAG_TISSUE=germinating seeds
TAG_SEQ=TCTGTGCGGG"
147 c 197 g 197 t
                                                                              /organism="Lactuca sativa"/cultivar="Salinas"
                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-912-020-325 (1-477) x BQ850159 (1-736)
                                                                                                                                                                                                                                                                                                                                                                                                                             2.49e-09
172.50
45.41%
31.63%
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                   for details.
Plate: QGB11
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                   195
                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
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                                                  FEATURES
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/strain="1712"
/db xref="taxon:73239"
/clone_"PyCPy36"
/clone_"PyCPy36"
/clone_lib="PyBS"
/dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
/note="Vector: pho-6AL4, At 20-25% parasitemia, blood was collected from BALB/CByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiccyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XNI and separated on a Sephacryl 5-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using ECORI-XNOI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA isolated.
                                                                                                                 BM169900 629 bp mRNA linear EST 04-DEC-2001
EST572423 PyBS Plasmodium yoelii yoelii cDNA clone PXCPY36 5' end,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       For clone info, please contact the Malaria Research and Reference Reagent Resource Center, ATCC http://www.malaria.mr4.org/mr4pages/index.html
                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 629)
Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.,
Fraser,C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 AAAAAAAAAACAGTGATGTTATGCCA-----TCAAATATAAAAGGTTTAATG 148
                                                                                                                                                                                                                                                                                             Plasmodium yoelii yoelii.
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Jane Cariton
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850,
Tel: 301-530-9319
Fax: 301-838-0208
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51
40
64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: carlton@tigr.org
                                                                                                                                                                                                                                      BM169900.1 GI:17303132
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171.50
46.43%
26.02%
7.17%
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FEATURES Location/Qualifiers source /organism="Physcomittella patens subsp. patens" /b_xref="taxon:145481" /clone="pph3121" /clone="ib="full length cDNA library, chloronemata and young gametophores" /tissue_Lype="mixture of chloronemata and young gametophores with 2 to 5 leaves" BASE COUNT 176 a 185 c 143 g 184 t lothers ORRGIN	Alignment Scores: 8.56e-09	Db 610 AAGATTGCTAAGAGTGCCGGTGTTCCTGTGATCATGGATGCTGGAGGTGCAGAAGGTCCT 551 Qy 183PheGluArgTyrArgGlyAlaThrLeuLeuThrProAsnLeuSerGluPheGlu 200		RESULT 12 B1944705 LOCUS LOCUS DEFINITION Sad41d05.y1 Gm-c1075 Glycine max CDNA clone GENOME SYSTEMS CLONE TD: Gm-c1075-538 5' similar to TR:095HH5 Q95HH5 F20D23.14 PROTEIN. ', mRNA sequence. B1944705 VERSION REYWORDS SOURCE SOURCE OKGANISM CANISM CANISM SET 29-NOV-2001 S1944705 SIGNATOR OF SIMILAR TO TR:095HH5 Q95HH5 F20D23.14 PROTEIN. CHAPTOR OF STEMPORE SOURCE OKGANISM CANISM CANICA CANISM CANI
Oy 317 AspThrGlyPheGlyValMetThrGluGluLeuLysLeuAlaValAlaAlaAla 335 149 AATAAAAATAAAGGTATATAGCAGCTTCACAATATTTATT	7 F D.F D .	OY 429 Leuvaltysely	BJ165221/C LOCUS BJ165221 full length cDNA library, chloronemata and young gametophores Physcomitrella patens subsp. patens cDNA clone pph3i21 3, mRNA sequence. 3, mRNA sequence. 3, mRNA sequence. BJ165221.1 GI:18333207 VERSION BJ165221.1 GI:18333207 BJ165221.1 GI:18333207 CRANISM Physcomitrella patens subsp.:patens. ORGANISM Physcomitrella patens subsp. patens. ORGANISM BYOPOPHY VII diplantae: Streptophyta: Embryophyta: Bryophyta; Bryopsida; Funarildae; Funariales; Funariaceae; Physcomitrella. Bryopsida; Funarildae; Funariales; Funariaceae; Physcomitrella. Carninci, P., Hayashizaki, Y., Shinozaki, K., Kohara, Y. and Hasebe. M. TITLE Comparison of the moss Physcomitrella patens genome with flowering	plants genome JOURNAL Unpublished (2002) COMMENT Contact: Tadasu Shin-i Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp A backbone of the vector is basically from pBluescript(KS), that was in vivo excised from a modified lPS phage vector Kob i Tec, Germany). 5' end of the cDNA that was digested with XhoI was 11gated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector. CDNA instert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated basically according to the method described in The Plant J 15, 707-720 (1998) Seki M. et al. Protonemata were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13-14 days under the continuous light.

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254 GlnGluValTyrAspValThrGlyAlaGlyAspThrValIleGlyValLeuAlaAlaThr 273
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Query Match:
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AUTHORS
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COMMENT
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BQ995975
                                                                                                                                                                                                                                                                                                                       ACCESSION
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Another The CDNA library was constructed from mRNA isolated from differentiating somatic embryos cultered on MSMGAC. The library was prepared using the Stratagene pBluescript II SK(+) library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the ECORI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were caractered into EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were caracterized into EcoLI ElectroMax DHIOB host cells. Thissue culture and library construction were performed by Francoise Thibaud-Nissen, and Anu Khana (Lila Vodkin lab,
                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801.For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="differentiating somatic embryos cultered on MSM6AC"
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 GATGGGCCCCTTCCACCACAATTATTGAATTTTGTTGATATTCTGAGTCCTAATGAAACT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 GluPheGluAlaValValGly---LysCysLysThrGluGluGluIleValGluArgGly 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 MetLysLeuIleAlaAspTyrGluLeuSerAla-----LeuLeuValThrArgSerGlu 234
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                                                                                                                                                                              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 AspPhe-----GluArgTyrArgGlyAlaThrLeuLeuThrProAsnLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Glycine max"
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/clone="GENOME SYSTEMS CLONE ID: Gm-c1075-538"
//clone_lib="Gm-c1075"
                                                                                          Unpublished (1999)
Context: Showmaker K/Public Soybean EST Project
Dublic Soybean EST Project
Washington University School of Medicine
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Conservative:
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103 c 134 g 1
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Location/Qualifiers
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166.50
49.64%
35.77%
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Best Local Similarity:
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/note="Vector: pBRCDNASFIAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_LIB=OG_EFGHJ lettuce serriola TAG_LISUE-chemical induction TAG_LISUE-chemical induction 126 c 190 g 162 t 8 others
                                                                                                                                                    EUSYSSY/S 686 bp mRNA linear EST 21-AUG-2002 QGG11110.yg.abl QG_EFGHJ Lettuce serriola Lactuca sativa cDNA clone QGG11110, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison Damme, M., Sabaudy, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K. Livingston, E., Jackson, L. and Bradford, K. Lompositae Genome Project Lettuce and Sunflower ESTs from the Compositae Genome Project Unpublished (2002)

Contact: Alexander Kozik [R.W.Michelmore]
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraccae; Lactuceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@tyg.corg [michelmore@vegmail.ucdavis.edu]
belongs to contig OG_CA_Contig5995, see http://cgpdb.ucdavis.edu/
274 LeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnAlaAla 290
                                                            435 TIGGITGAGGGCAAGICCAAAAGGAATGCCICAGATITGCTGCTGCTGCG 485
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/clone_lib="QG_EFGHJ lettuce serriola"
/lab_host="E.coli"
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Matches:
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Location/Qualifiers
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/db_xref="taxon:4236"
                                                                                                                                                                                                                                                                                                                                                                                                  Lactuca sativa
Eukaryota; Viridiplantae;
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Best Local Similarity:
Query Match:
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ORIGIN
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grusak M.A., Samac, D.A., Town, C.D., Van Aken, S., Utterback, T., Cho, J. and Fraser, C.M.

"J. and Fraser, C.M.

ESTS from developing reproductive tissues of Medicago truncatula Unpublished (2001)

Contact: Michael A. Grusak

USDA/ARS Children's Nutrition Research Center

Baylor College of Medicine
                                                                                                                                                                                                  303
                                                                                                                                           243
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                                                                                                                                                                                                                                         405 AlaValAspTrpValVal------SerPheGluGluAspThrProGlnArg 419
                                                                                                                                                                                                                                                                                                                                                            420 LeuIleAlaGlyIleLeuPro-AspLeuLeuValLysGlyGlyAspTyrLysProGluGl 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                         439 uIleAlaGlySerLysGluValTrpAla-----AsnGlyGlyGluValLeuValLe 456
                                                        324
                                                                                                            325 GluGluGluLeuLysLeuAlaValAlaAlaAlaArgLysArgGlyGluLysValValMet 344
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                                                                                                                                                                                                                                                                                 385 GlyAspSerArgProValAsnProLeuGluGlnArgMetIleValLeuGlyAlaLeuGlu 404
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                          76 AAGATGGGTTCGGATACA-----GGTCTAGAGAACTCGAAGCGGTTTCCNNCG 123
                                                                                 124 ACATGGTTGATCGGAGGTTGGTGGCAGGCTATCGGTTATGGGGTTATGCGCTGCTTGG 183
                                                                                                                                                                     CCGGAGCTCTCCCCTCTGAGTATTGTTGGGAGGAAGAGAAGAGGCCCCATTCGTGTATAC
                                                                                                                                                                                                                            LysLeuGlyAspArgLeuIleValAlaValAsnSerAspAlaSerThrLysArgLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                   TIGR sequence name: MTOAD46TK
More information is available at: www.medicago.org
seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
1. 729
 LysLeuGlyThrSerThrValSerProIleGluLeuGluAsnAlaValArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1100 Bates Street, Houston, TX 77030-2600, USA Tel: 713-798-7044
Fax: 713-798-7078
                                                        -------GlyArgAlaAspThrGlyPheGlyValMet-
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B394859e
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BI308004.1 GI:14982331
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/clone="popp-large" |
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/dev_stage="Immature pods, ranging in age from 15 to 30
days_after pollination" |
/dev_stage="Immature pods, ranging in age from 15 to 30
days_after pollination, were collected from greenhouse-grown plants. At harvest, seeds were remcved from pods and isolated pod walls were collected and immediately frozen in liquid nitrogen. Pod walls were pooled for mRNA extraction. CDNA was prepared from polya+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Glapapeck III Gold packaging extracts. Plasmids coutaining cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propogated in XLOLR cells."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 ATTATTCATGGGGACGAT-----CCTTGTGTTCTTCCTGATGGAACTGATGCTTATGCT 477
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46
31
55
14
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Mismatches:
Indels:
/organism="Medicago truncatula"
/cultivar="A17"
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Matches:
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                                  /cultivar="A17"
/db_xref="taxon:3880"
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158.00
52.74%
31.51%
6.60%
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Location/Qualifiers

1. 609

(Apple 1. 609)

/ Organism="Medicago truncatula"

/ Ab_xref="taxon:3880"

/ Clone="NF014A091N"

/ Clone="nF014A091N"

/ Clone="nF014A091N"

/ Lissue_type="locat and systemic leaves"

/ Assue_type="locat and systemic leaves from fully expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled.

### Page 152 g 202 t 5 others
                                                                                                                                Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library
Unpublished (2000)
                                          Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                Contact: Korth K, bathology between the contact of Plant Pathology University of Arkansas 217 Plant Science Building, Fayetteville, AR 72701, USA 7e1: 501 575 5191
Fax: 501 575 7601
Bmail: kkorth@comp.uark.edu
Enser: Length: 609 Std Error: 0.00
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Matches:
Conservative:
Mismatches:
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157.00
52.45%
32.17%
6.56%
                        Medicago truncatula
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Best Local Similarity:
Query Match:
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Db 455 CATGCCAAAAAGGCTGGCCGCTATAAACAGATTAAGCGCACGGAAGGAGTTTCCAGCACT 514

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Db 515 GATATTGTG 523
Search completed: November 26, 2002, 22:39:52
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Total number

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Scoring table:

Perfect score:

Sequence:

OM protein

Run on:

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APPLICANT: Mathan Dr., Michael J.
APPLICANT: Mathan Dr., Christopher P.
APPLICANT: Conner Mr., Christopher P.
APPLICANT: Hiethoff Mr., Douglas M.
TITLE OF INVENTION: METHOD AND PROBES FOR THE IDENTIFICATION
TITLE OF INVENTION: OF MICROBIAL GENES SPECIFICALLY INDUCED DURING HOST
TITLE OF INVENTION: INFECTION
NUMBER OF SEQUENCES: 255
CORRESPONDENCE ADDRESS:
                                                                                                  Sequence 1, Appropries 5, Appropries 5, Appropries 43, 1
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Sequence 6, A
Sequence 6, A
Sequence 6, A
Sequence 3, A
Sequence 16,
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Sequence 7, A
Sequence 9, A
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US-09-199-637A-1

US-08-18-01-2746

US-08-18-01-2746

US-08-18-01-1

US-08-18-11-1

US-08-18-198-1

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US-08-18-198-1

US-08-18-13-43

US-09-265-315-43

US-09-265-315-43

US-09-265-315-43

US-08-28-2618-6

US-08-58-2618-6

US-08-58-2618-6

US-08-457-348-6

US-08-457-348-6

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US-08-457-358-16

US-08-479-614-3

US-08-955-957A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZUP: 60302
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,155B |
FILING DATE: 17 - MAX-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hrisman, Bynum & Johnson,
Fifteenth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 185, Application US/08651155B Patent No. 6365401 GENERAL INFORMATION:
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NAME: Petersen Mr., Steven C.
REGISTRATION NUMBER: 36,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/546-1300
TELEFAX: 303/449-5426
TELEXX: ABA1475
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1900 Fifteent
    CITY: Boulder STATE: CO
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-Q-Cqqn2_1/YOSPO_2pool/USQ9912020/runat_25112002_091429_24273/app_query.fasta_1.647
-Q-Cqqn2_1/YOSPO_2pool/USQ9912020/runat_25112002_091429_24273/app_query.fasta_1.647
-Q-Cqqn2_1/YOSPO_2pool/USQ9912020_YOSPO_2
-LOSPEXT-0 -UNITS-bits -START-1 -END-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DGO-ADCALIGN-200 -THR_SCOREE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15
-UOSPE-LOCAL -OUTFMY-pto -NORM-ext -HEAPSTEE-500 -MINLEN-0 -MAXLEN-2000000000
-USER-USG9912020_GCGN_1_138_Grunat_25112002_091429_24273 -NCPU-6 -ICPU-3
-NOA_XLDXY -NO_MAND -LARGEDDERY -NGC_SCORES-0 -WAIT -LONGLOG -DEV_TIMBOUT-120
-WARN TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
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1 MKVTLPEFERAGVMVVGDVM.....FEDGCSTINIIKKIQQDKKG
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                      GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                  nucleic search, using frame_plus_p2n model
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US-08-651-155B-186
US-08-134-001C-1684
US-08-920-812-19
US-08-920-827-19
US-08-920-828-19
US-08-136-577C-19
US-09-134-001C-2723
US-09-134-010C-2723
US-09-139-637A-280
US-09-199-637A-272
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Patent No. 6365401.
GENERAL INFORMATION:
APPLICANT: Mahan Dr., Michael J.
APPLICANT: Conner Mr., Christopher P.
APPLICANT: Highloff Mr., Douglas M.
APPLICANT: Highloff Mr., Douglas M.
TITLE OF INVENTION: OF MICROBIAL GENES SPECIFICALLY INDUCED DURING HOST TITLE OF INVENTION: INPECTION
TITLE OF INVENTION: 1NFECTION
TITLE OF INVENTION: 1NFECTION
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AAGGTAAATACCGTTGAGGAACGCCCGGCGGCGCGCGCAACGTGGCGATGAACATTGCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TGCTCTGGGAGCGAACGCCGTCTGGTCGGCCTGACGGGTTATTGATGACGCCGCGGCGC- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 laLeuSerLysSerLeuAlaAspValAsnValLysCys-AspPheValSerValProThr 100
                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                  42 LysValAsnThrIleGluGluArgProGlyGlyAlaAlaAsnValAlaMetAsnIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 pPheGluGluGlyPheGluGlyValAspProGlnProLeuHisGlu 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297 -TTTGAAGAGGCTTTGAGGAT --- GACCGCAAGCCGTTGCATGAG 338
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                                                                                                                                                                                                                                                                                                                                   US-09-912-020-325 (1-477) x US-08-651-155B-185 (1-347)
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Mismatches:
Indels:
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1900 Fifteenth Street
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Matches:
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APPLICATION NUMBER: US/08/651,155B
FILLIN DATE: 17-MAY-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                      MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                             411.50
88.14%
83.90%
17.20%
                                LENGTH: 347 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
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US-08-651-155B-186
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STREET: 19'
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GENERAL INFORMATION:

APPLICANT: LYAN DOUGETLE-Stamm et al
APPLICANT: LYAN DOUGETLE-STAMM et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCOC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPBUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-08-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 IleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      327 GluLeuLysLeuAlaValAlaAlaAlaArgLysArgGlyGluLysVa.LValMetThrAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ATCGGCGTGCTGGCGGCGACCTG-GCCGCGGGAAATACCCTGGAAGAGGGGTGTTATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    347 GlyValPheAspIle---LeuHis-----AlaGlyHisValSerTyrLeu 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 ---GCGTTCGATATCTGACGGCATTATGACGCAACTGGACCTATCGGATACTTA 281
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Staphylococcus epidermidis
            NAME: Petersen Mr., Steven C.
REGISTRATION NUMBER: 36,238
REFERENCE/DOCKET NUMBER: 17060
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/546-1300
                                                                                                                                TELEX: ABA1475
INFORMATION FOR SEQ ID NO: 186: SEQUENCE CHARACTERISTICS: LENGTH: 294 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                 1.33e-20
263.00
79.598
73.478
10.998
ATTORNEY/AGENT INFORMATION:
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SEQ ID NO 1684
LENGTH: 948
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Best Local Similarity:
Query Match:
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CAAGCATTAAAATTGCTCGTAAACAAATATCACTACTGTATTAAATCCTGCACGGCA 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTGATATGAAAGAAACAACAACATATTTTCTCGATTTAGGTATATCTGCAGTATTAATT 690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------LysGlyThrAspPheGluArgTyrArgGlyAlaThr 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 GATAAATTTCTT-----AATGTTAAAAGGTTTCCAAAA---CCCGGTGAGACATTA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 GCTAGTAGATTAGCAGCAGATACAACATTATCAGTAAAGTTGGTAAAGATGGCAATGCT 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaLeuValLeuSerAspTyrAlaLysGlyAlaLeu------AlaSerValGln 161
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                                                                                                                                                                                                                                                                                                                                                                                                  115 CATATTAATCAAGCTCAAAAGGAGTTTGGTGGGGGCAAGGGÄGCCAATCAAGCCATAGCA 174
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7 AAAGTAGGTGAAGTTGAAATGAATAAAATAAAGTGATTGTAATTGGATCAACAAATGTA
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748 GCGTGTAATGTAAAAGCAATAGATACGACAGCAGCAGGAGATACATTATAGGTGCTTTT
                                                                                                                                                                                                                                                                                                                                                      42 LysValAsnThrIleGluGluArgProGlyGly-----AlaAlaAsnValAlaMetAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                              60 IleAlaSerLeuGlyAlaAsnAlaArgLeuValGlyLeuThrGlyIleAspAspAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 AACTTTATATTGGAA-----------GATTTCAAAAAGCAGGT
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295 GADAGTGAAGAAACTGGGGCAAGCATTATCACTGTTGATGAAGCAGGACAAAATACGATT
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                                                                                                                                                                                                                                                                   22 AspArgTyrTrpTyrGlyProThrSerArgIleSerProGluAlaProValProValVal
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    .Matches:
Conservative:
Mismatches:
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                         Percent Similarity:
Best Local Similarity:
                                                                   Query Match:
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South Wacker Drive
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                                                                                                                                                                                                                                                                                                                         COUNTRY: United States of America ZIP: 60606-6402
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APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTONENY/AGENT INFORMATION:
NAME: Rib-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,812
FILING DATE: 29-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                            Sequence 19, Application US/08920812 Patent No. 5763188 GENERAL INFORMATION:
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STRAIN: Clinical Isolate EC-39
                                                                                                                                                                                                                                                    3: Marshall, O'Toole,
6300 Sears Tower, 233
                                                                                                                                 APPLICANT: Ohno, Tsuneya
APPLICANT: Mtsuhisa, Akio
APPLICANT: Gustantia, Hirotsugu
APPLICANT: Eds, Soji
TITLE OF INVENTION: Probe for NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION
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INFORMATION FOR SEQ ID NO: 19:
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EDNESS: double
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Best Local Similarity:
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STREET: 63
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2132 ACCACTATCAGGTTGCATTT-GGCGGCAAAGGCGCGAATCAGGCTGTGGGCTGCTGGGCGT 2190
                                                                 2455 -----CTGGAATCACCACTCGAAAGTGTGATGGCAGCGGCGAAAATCGCCCATCAAAAT 2508
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2629 ATGATGAAGATGCAAGGCGGGGGGGGGAGGTACTTCATGAAAAAGGTATCCGTACTGTAC 2688
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|2278 GATATTACTCCGGTCAGCGTATCAAGGCGAATCAACAGGTGTGGCGCTGATTTTTGTT 2337
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                                    63 LeuGlyAlaAsnAlaArgLeuValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLeu
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2866 CTGCCGCTGCGATTGCCGTAACACGTAAAGGCGCACAACCTTCCGTACCG 2915
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APPLICANT: Watsuhisa, Akio
APPLICANT: Uehara, Hirotsugu
APPLICANT: Uehara, Hirotsugu
APPLICANT: Gai, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disea
NOMBER OF SEQUENCES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                2251 CGCCAGCACTCGCCACTGATAACATT-----
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X: United States of America
60606-6402
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Patent No. 5770375
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2338 AATGGC---GAAGGTGAGAATGTCATCGGTATTCATGCCGGCGCTAATGCTGCCCTTTCC 2394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrileThriysLeuArgValLeuSerArgAsnGlnGlnLeuIleArgLeuAspPheGlu 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 LeuProGluPheGluArgAlaGlyValMetValVal---GlyAspValMetLeuAspArg 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 TyrTrpTyrGlyProThrSerArglleSerProGluAlaProValProValValLysVal
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79
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156
37
                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-912-020-325 (1-477) x US-08-920-827-19 (1-3796)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches:
Indels:
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Matches:
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                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                           APPLICATION NUMBER: US/08/920,827
FILING DATE: 29-AUG-1997
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Escherichia coli
STRAIN: Clinical Isolate EC-39
                                                                                                                                                                                                                                                                  NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 1
TELECOMMUNICATION INFORMATION
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 3796 base pairs
nucleic acid
EDNESS: double
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39.62%
24.84%
6.31%
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Best Local Similarity:
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STRANDEDNESS:
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MOLECULE TYPE:
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                                                                                                                   -----CTGGAATCACCACTCGAAAGTGTGATGGCAGCGGCGAAAATCGCCCCATCAAAAT 2508
                                                                                     170 aGlyvalProvalLeuIleAspProLysGlyThr-AspPhe---GluArgTyrArgGlyA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                             etProThrGlnAlaGlnGluValTyrAspValThrGlyAlaGlyAspThrValIleGlyV 269
151 AspTyrAlaLysGlyAlaLeuAlaSerValGlnGlnMetIleGlnLeuAlaArg-LysAl 170
                                                                                                                                                                                                    2569 TGGACATTATTACGCCAAACGAAACGGAAGCAGAAAAGCTCACCGGTATTCGTGTTGAAA
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                                                                                                                                                                          189 laThrLeuLeuThrProAsnLeuSerGluPheGluAlaValValGlyLysCysLysThrG
                                                                                                                                                                                                                                                                209 luGluGluIleValGluArgGlyMetLysLeuIleAlaAspTyrGluLeuSerAlaLeuL
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APPLICANT: Matsuhisa, Akio
APPLICANT: Watsuhisa, Akio
APPLICANT: Uebara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289 laAlaAlaGlyValValValGlyLySLeuGlyThrSerThrValSerPro 305
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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COUNTRY: United States of America,
ZIP: 60606-6402
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FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: RID-Laures, Li-H9ien
REGISTRATION NUMBER: 33,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/921,177 FILING DATE: 29-AUG-1997 CLASSIPTCATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 3796 base pairs
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2509 AAAAACTATCGTTAACCCGCTCCGGCTCGCGAACTTCCTGACGAACTCTGCGCTG 2568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 AspTyrAlaLysGlyAlaLeuAlaSerValGlnGlnMetIleGinLeuAlaArg-LysAl 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 LeuProGluPheGluArgAlaGlyValMetValVal---GlyAspValMetLeuAspArg 23
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Mismatches:
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                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                       ORGANISM: Escherichia coli
; STRAIN: Clinical Isolate EC-39
US-08-921-177-19
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                            151.00
39.62%
24.84%
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Best Local Similarity:
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No.:
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2191 AGCGGTGCGAATATCGCGTTTATTGCCTGTACGGGTGATGACAGCATTGGTGAGAGCGTT 2250
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--CTTAATCTTCAATCTTTCCTACTCCAGGCGAAACGTAACCGGTA 2131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2395 CCGGCGCTGGTGGAAGCGCAACGTGAGCGTATTGCCAACGCGTCAGCATTATTAATGCAG 2454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2746 TTCCTGGATTCCGGGTGCAGGCTGTCGATACCATTGCTGCCGGAGATACCTTTAACGGTG 2805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 laThrLeuLeuThrProAsnLeuSerGluPheGluAlaValValGlyLysCysLysThrG 209
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                                                                                                            2132 ACCACTATCAGGTTGCATTT-GGCGGCAAAGGCGCGAATCAGGCTGTGGCTGCTGGGGGGT
                                                                                                                                                                        LeuGlyAlaAsnAlaArgLeuValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLeu
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                                                      44 AsnThrIleGluGluArgProGlyGly---AlaklaAsnValAlaMetAsnIleAlaSer
                                                                                                                                                                                                                                                                                                                                             251 CGCCAGCAGCTCGCCACTGATAACATT
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Patent No. 5853998
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Matsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Uchara, Hirotsugu
APPLICANT: Uchara, Hirotsugu
APPLICANT: Uchara, Hirotsugu
APPLICANT: Uchara, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Dis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Bory
STREET: 6300 Sears Tower, 233 South Macker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 6300 $ CITY: Chicago
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US-08-920-828-19
2084 ATT---
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2746 TTCCTGGATTCCGGGTGCAGGCTGTCGATACCATTGCTGCCGGAGATACCTTTAACGGTG 2805
                                                      269 alLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnA 289
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                                                                                                               2806 CGTTAATCACGGCATTGCTGGAAGAAAACCATTGCCAGAGGCGATTCGTTTTGCCCATG
                                                                                                                                                                                                                                                                                                                              Sequence 19, Application US/08362577C
Patent No. 5807673
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Webara, Hirotsugu
APPLICANT: Eda, SO,1
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Matshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                         laAlaAlaGlyValValValGlyLysLeuGlyThrSerThrValSerPro 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 27-MAR-1995
CLASSIFICATION: 536
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: 111inois
COUNTRY: United States of America
2IP: 60606-6402
COMPUTER READABLE FORM:
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Clinical Isolate EC-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: RID-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 1903
TELECOMUNICATION INFORMATION:
TELEPHONE: 312/474-6400
TELEPAX: 312/474-6408
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
EDNESS: double
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Best Local Similarity:
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MOLECULE TYPE: G
ORIGINAL SOURCE:
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STATE: Illino
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CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14 NUMBER OF SEQ ID NOS: S674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2723, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:
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150.00
54.68%
33.81%
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                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, «Version #1.25
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/08/920,828
FILIG DATE:
FLIGH DATE: 435
CLASSIFICATION: 435
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                             NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
TELECOMOUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFRAX: 312/474-0448
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                                                                                                                                                                                  CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
Illinois
: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Escherichia coli
STRAIN: Clinical Isolate EC-39
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151.00
39.62%
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STRANDEDNESS: double
TOPOLOGY: linear
                                60606-6402
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Best Local Similarity:
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APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: UCCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1569 TGGACATTATTACGCCAAACGAAAGCAGAAAGCTCACCGGTATTCGTGTTGAAA 2628
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                                                                        2395 CCGCCCTGGTGGAAGCGCAACGTGAGCGTATTGCCAACGCGTCAGCATTATTAATGCAG 2454
                                                                                                                                                                                                                                                                                          170 aGlyValProValLeuIleAspProLysGlyThr-AspPhe---GluArgTyrArgGlyA 189
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-----SerIle3lyAlaLeuValLeuSer 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 AlaAsnAlaArgLysLeuGlyAspArgLeuIleValAlaValAsnSerAspAlaSerThr 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 629 ATGATGAAGATGCAGCGAAGGCGGCGCAGGTACTTCATGAAAAGGTATCCGTACTGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 alLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 AspTyrAlaLysGlyAlaLeuAlaSerValGlnGlnMetIleGlnLeuAlaArg-LysAl
                                                                                                                                                                                                                                                                                                                                                                  2509 AAAAACTATCGTTCGCTTAACCCGCTCCGGCTCGCGAACTTCCTGACGAACTCTGCGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2866 CTGCCGCTGCGATTGCCGTAACACGTAAAGGCGCACACATCC3TACCG 2915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289 laAlaAlaGlyvalValValGlyLysLeuGlyThrSerThrValSerPro 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-912-020-325 (1-477) x US-09-134-001C-2723 (1-414)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
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Indels:
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Matches:
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:::::	Score: Percent Best Loc Query Ma	Score: Percent Similari Best Local Simil Query Match:
	. DB:	DB: US-09-912-020-3:
GlyAlaLeuGlualaValaspTrpValValSerPheGluGluAspThrProGlnArgLeu 420 :::::: ::: GAGTTATTAGTTATTAGATAGGGAAGGGGGACAGAAAGAA		
IlealaGlyIleLeuProAspLeuLeuValLySGlyGlyAspTyrLySProGlu 438 :::	oy y	
GluileAlaGlySerLysGluValTrpAlaAsnGlyGlyGluValLeuValLeuAsnPhe 458 		
459 GluAspGlyCysSerThrThrAsnIleIleLysLysIleGlnGlnAspLysLysGly 477 		
RESULT 10 US-09-453-702B-149/c	qa do	9767 ATAGGT 90 Asnval
Sequence 14-7, Application 05/03455702B Patent No. 6365723 GENERAL INFORMATION:	5 qq	9707 GGAGTC
APPLICANT: Blattner, Frederick R. Burland, Valerie	Qy 4	109 ValLet
#		
TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157 NUMBER OF SEQUENCES: 265	6 G G	
CORRESPONDENCE ADDRESS: ADDRESSEE: Quartles & Brady comprem 1 Court Displace Ct.	Qy	136 ArgIle
SIREDI: 1 SOULH FINCKHEY SLIGEL CITY: Madison STAFF: WI	o qa	9536
COUNTRY: US ZIP: 53701-2113	Qy	156 AlaLe
COMPUTER FADABLE FORM: WEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage	o qa	9494 GCATT
	Oy	176 IleAsp
TWARE: Word Perfect 8.0 APPLICATION DATA:	o qa	9446 TTCGA
APPLICATION NUMBER: US/09/453,702B FILTING DATE: 03-Dec-1999	٥y	183 PheGlu
CLASSIFICATION: <unknown></unknown>	o qa	9386 CGGCAC
APPLICATION NUMBER: 60/110,955	QY	203 ValGly
ATTORNEY/AGENT INFORMATION: NAME: Seav. Nicholas I	o qu	9326 AGTGG
REGISTRATION NUMBER: 27386	Qy	223 TyrGlu
TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:	o qa	9278 TATGAC
TELEFICATE: (008) 251-9166 TRECEPARATON EDG SEC IN NO. 140.	δŏ	243 GlyLys
SEQUENCE CHARACTERISTICS:	5 qq	9218 GGACA
LENOIH: 12804 TYPE: nucleic acid equannennes: double	Qy	263 GlyAsp
Standburgss: double TOPOLOGY: linear	5 qq	9161 GGAGA
SEQUENCE DESCRIPTION: SEQ ID NO: 149: US-09-453-702B-149	Qy	282 Glu
	5 qa 	9101 GAGAGA
3.92e-05 Length: 12804	٥y	297 LysLe

		30 9867	50	69 9768	89 9708	108	121 9594	135 9537	155 9495	175 9447	182 9387	202 9327	222 9279	242 9219	262 9162	281 9102	296	
Matches: 81 Conservative: 49 Mismatches: 136 Indels: 57 Gaps: 15	9-453-702B-149 (1-12804)	spValMetLeuAspArgTyrTrpTyrGlyProThrSer ::::: ATGCGGTCGTAGAT	alProvalValLysValAsnThrlleGluGluArgPro	GlyGlyAlaAlaAsnValAlaMetAsnIleAlaSerLeuGlyAlaAsnAlaArgLeu 	AlaAlaArgAl TTTGGTGCAT	AsnvalLysCysAspPheValSerValProThrHisProThrIleThrLysLeuArg	GGGAACGTTCATTTACGTTTATGGTCCGCCCCAGTGCC	TTGCCCTGCTGG	aLeuSerSerIleGlyAlaLeuValLeuSerAspTyrAlaLysGly - -CTCTGTTCAATTGGGTTGTCTGCGGGGCCTTCGCGTACCAGC	IleGl	ATCTATGGCAAGACGAGCATTTGCTCCGCTTGTGTTTG	heGluArgTyrArgGlyAlaThrLeuLeuThrProAsnLeuSarGluPheGluAlaVal:::: ::: ::::::::::::::::::::::	luGluileValGluArgGlyMetLysLeuileAlaAsp :::	yrGluLeuSerAlaLeuLeuValThrArgSerGluGlnGlyMetSerLeuLeuGlnPro :::::: ATGAGATCGCCATGCTGTTGGTGACTAAAGGTGCAGAAGGGGTGGTGGTGGTGTTGTTGGA	GlyLysalaProLeuHisMetProThrGlnalaGlnGluValTyrAspValThrGlyAla ::	IleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGlu 	lu	erProlleGluLeuGlu 309
146.50 Similarity: 39.04% cal Similarity: 24.32% ttch: 6.12%	120-325 (1-477) x US-0	AlaGlyValMetValValGlyAspValMetLeuAsp 	ArgileSerProGluAlaProValProValValLysV. ::: :::CTCTTGCCAGAATCAGACGGGGGGGGTACTGCCTT	lyGlyAlaAlaAsnVali GCGGCGCCAGCTAACGTT	ValGlyLeuThrGlyIleAspAsp ::: ATAGGTCGGGTGGGGGATGATCCT	AsnValLysCysAspPheValSerV GGAGTCGATATCACGTATCTGAAGC	ValleuSerArgAsnGlnGln	GluGluGlyPheGluGlyValAsp ::: GATCTTTTTTAGAGACGACAGAC	ArgIleAsnGlnAlaLeuSer CTCTGT	AlaLeuAlaSerValGlnGlnMetIl. CATTTACTGCGATGACGGAGATC	IleaspProLysGlyThrasp TTCGATCCCAATATTCGTGAAGATCT	PheGluArgTyrArgGlyAlaThrLeuLeuThr: :::::: :::::: CGGCAGGCGCTACACTGGCGGATGTCGTCAAG	ValG1yLysCysLysThrG1uG1uG1uI1eVal(:: :: AGTGGAAAACACAGAACGATCGGGATATA	TyrGluLeuSerAlaLeuLeu' :::::: TATGAGATCGCCATGCTGTTG	YLYSA aProLeuHisMet :: GACAAGTTCACCATTTT	GlyAspThrVallleGly GAGATGCGTTCGTTGCCGGG	GluAla(GAGAGAGAATGCGACGAATT)	LysLeuGlyThrSerThrValSerProIl
π. ξ. ğ. ğ.	09-912-0	11 P	31 A 9866 -	51 G 1 9827 G	70 7	90 4	109 \	122 C	136 A	156 A	176 1	183 F	203 7	223 1 9278 1	243 G	263 (9161 (282 (297 I
Score Percel Best Douery	us-(Qy Db	QY Db	Qy Db	Qy	Qy Db	Qy Db	Qy Db	Qy	Ογ Db	Qy Db	OY Dp	oy Ob	Oy Dp	Q Dp	O _Y	QY	οy

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163 MetileGlnLeu-----AlaArgLysAlaGlyValProValLeuIlcAspProLysGly 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 LeuIleArgLeuAspPheGlu-----GluGlyPheGluGlyValAsp 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGCGCGCCGAGGAAGGCAAGCTCGACCCGGTGATCGGTCGCGACGACGACGAGGATCCGCCGG 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CICAACCAGGCIGACCGCCIGGCCCAGCAGGGCGACCAGTICAICICCAGCGAGCIG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProGlnProLeuHisGluArgIleAsnGlnAlaLeuSerSerIleGlyAlaLeuValLeu 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlaAsnValAlaMetAsnIleAlaSerLeu-----GlyAlaAsnAlaArgLeuValGly
                                                                      GENERAL NO. 0353411.

GENERAL NO. 0353411.

APPLICANT: Ausubel, Frederick
APPLICANT: Goodman, Howard M.
APPLICANT: Rahme, Laurence G.
APPLICANT: Rahme, Laurence G.
APPLICANT: Tan, Man'Wah
APPLICANT: Tan, Man'Wah
APPLICANT: Toongalls, John
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/361002
CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
PRIOR FILING DATE: 1998-11-25
NUMBER OF SEQ ID NOS: 437
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 280
LENGTH: 2580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProvalvalLysValAsnThrIleGluGluArgProGlyGlyAla--
                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-912-020-325 (1-477) x US-09-199-637A-280 (1-2580)
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                     Sequence 280, Application US/09199637A Patent No. 6355411
                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa US-09-199-637A-280
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138.50
39.38%
25.15%
5.79%
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Best Local Similarity:
Query Match:
DB:
                                         US-09-199-637A-280
                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                            TYPE: DNA
         9041
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1312 GAC------CAGAGCCACCAGGAAGCGCCTGGCCAAG-----CTGGAG 1350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          355 GlyHisValSer----TyrLeuAlaAsnAlaArgLysLeuGlyAspArgLeuIleVal 372
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               642
                                                                                                                                                                                                                                                                                                                                               221 AlaAspTyrGluLeuSerAlaLeuLeuValThrArgSerGluGlnGlyMetSerLeuLeu 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyAlaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeu 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       913 AAGCCGGCTCTGGCGCGCGCGGCGACTGCTCGTCGTGCTACTA------CC 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   319 lyPheGlyValMetThrGlu-GluGluLeuLySLeuAlaValAlaAlaArgLySArg 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                339 GlyGluLys......ValValWalMetThrAsnGlyValPheAspIleLeuHisAla 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         373 AlavalAsnSerAspAlaSerThrLysArgLeuLysGlyAspSerArgPro-----Val 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trp---AlaasnGlyGlyGluValLeuValLeuAsnPheGluAspGlyCysSerThrThr 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluGluAlaCysPhe-PheAlaAsnAlaAlaAlaGlyValValValGlyLysLeuGlyTh 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspValThr
                                                                                                                                                                                                     685 ATCAACGGCGAAGTGCCGGACGGCCTCAAGGACAAGCGCCTGCTGGCCCTGGACATGGGG
                                                                                                                                                                                                                                                     AlaValValSlyLysCysLysThrGluGluGluIleValGluArgGlyMetLysLeuIle
                                                            181 ThraspPheGluArgTyrArgGlyAlaThrLeuLeuThrProAsnLeuSer-----
                                                                                                                                                                                                                                                                                                                                                                                                   -----CTGAAGGCGGTCCTC-----AACGAACTGGGCAAG-----
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; Sequence	272, Applica	uence 272, Application US/09199637A	
Patent N	lo. 6355411		
ENERAL INF APPLICANT:	GENERAL INFORMATION: APPLICANT: Ausubel,	, Frederick	
APPLICANT:	Goodmar	•	
APPLICANT:	Kanme, Mahajar	Mahajan-Miklos, Shalina	
APPLICANT: APPLICANT:	Tan,	Man-Wah Hui	
APPLICANT:		d, Eliana	
	Ę	s, John	
TITLE	OF INVENTION:	ENTION: SEQUENCES AND USES THEREOF	
TLE RE	FILE REFERENCE: 007 CURRENT APPLICATION	FILE REFERENCE: 00/86/361002 CURRENT APPLICATION NUMBER: 0S/09/199,637A	
CURRENT	FILING DATE:	: 1998-11-25	
PRIOR A	PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1997-1	NMBER: 60/066,517 1997-11-25	
NUMBER O SOFTWARE	NUMBER OF SEQ ID NOS: SOFTWARE: FastSEQ fo	S: 437 for Windows Version 4.0	
EQ ID NO 2 LENGTH: 2	Q ID NO 272 LENGTH: 2970	•	
ORGANISM: 09-199-637		Pseudomonas aeruginosa N-272	
Alignment	Scores:	- 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1	
Score: Percent Si	.milarity:	Denyth: Matches: Conservative:	
Local y Matc	Best Local Similarity: Query Match: DB:	: 25.15% Mismatches: 179 5.79% Indels: 132 4 Gaps: 28	
US-09-912-	-912-020-325 (1-47	(1-477) x US-09-199-637A-272 (1-2970)	
39	ProvalvalLys	ProValValLysValAsnThrIleGluGluArgProGlyGlyAla	53
2859	CCGGTGCACCTGC	CGGTGCACCTGCTTTCCGCCCTGCTCGAGCAGCAGAGCGGTTCGATCAAGCCCCTGCTG	cccrccrc 2800
54	AlaAsnValAlaN	AlaAsnvalAlaMetAsnIleAlaSerLeuGlyAlaAsnAlaArgLeuValGly	euValGly 71
2799	ATGCAGGTCGGCJ	ATGCAGGTCGGCTTCGATATCGCCGCCCTGCGCGCGCCTCAACAAAAAAACGACGCG	rcgaccc 2740
72	LeuThrGlyIle-	Aspaspala	AlaArgAla 81
2739	CTGCCGAAGATCC	CTGCCGAAGATCCAGAGCCCGACCGCGACGTGAACCTGTCCCAGGATCTCGCACGCCTG	CACGCCIG 2680
83	LeuSerLysSer-	LeuAlaAspValAsnValLysCysAspPhe	ysAspPhe 95
2679	CTCAACCAGGCTC	CTCAACCAGGTGACCGCCTGGCCCAGCAGAAGGGCGACCAGTTCATCTCCAGCGAGCTG	GCGAGCTG 2620
96	ValSerValPro	ValSerValProThrHisProThrIleThrLysLeuArgValLeuSerArgAsnGlnGln	snGlnGln 115
2619	GTATIGCTGGCCC	GGTCGGCAAGC	GCCAGGGC 2560
116	LeuIleArgLeuAspPheGlu-	AspPheGluGluGlyPheGluGlyValAsp	lyvalAsp 129
2559	GTGTCGCGCAAGG	:::	::: CGTGAAC 2500
130	ProGlnProLeuF	ProGlnProLeuHisGluArgIleAsnGlnAlaLeuSerSerIleGlyAlaLeuValLeu	euValLeu 149
2499	GACCCGAACC	-GACCCGAACGTCGAGGAGTCGCGCCAGGCGCTGGACAAGTACACCGTCGACATGACC	ACATGACC 2443
150	SerAspTyrAlai	SerAspTyrAlaLysGlyAlaLeuAlaSerValGlnGlnGln :::	alGlnGln 162
2442	AAGCGCGCCGAGC	aagcgcgcgaggaaggcaagctcgacccggtgatcggtcgcgacgacgagatccgcgg	TCCGCCGG 2383
163	MetIleGlnLeu-	<pre>MetileGlnLeuAlaArgLysAlaGlyValProValLeuIleAspProLysGly </pre>	roLysGly 180
2382	ACCATCCAGGTCC		AACCCGGC 2323

δy	181	rgGlyAlaThrLeuLeuThrPrcAsnLeuSe
qq	2322	GTC
Qy	198	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
qq	2280	ည္
Qy	201	uGluGluIleValGluArgGlyMetLysLeuI
qq	2220	1
Qy	221	aAspTyrGluLeuSerAlaLeuLeuValThrArgSerGluGlnGlyMetSerL
QQ	2175	
Qy	241	GlnProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspValThr 260
QQ	2145	CAGGAAGGCCGGGTCATCCTGTTCATCGACGAACTGCACACCATGGTC 2098
Οy	261	7
Op	2097	GGCGCCGGCAAGGCGGAAGGTGCCATGGACGCGGAACATGCTC 2053
Οy	281	GluGluAlaCysPhe-PheAlaAsnAlaAlaGlyValValValValGlyLysLeuGlyTh 300
qq	2052	AAGCCGGCTCTGGCGCGCGGCGGCTGCACTGCGTCGGTGCTACTACC 2005
Qy	300	rSernhr-ValSerProlleGluLeuGluAsnAlaValArgGlyArgAlaAspThrG 319 ::
QQ	2004	CICGACGAGIATCGCCAGIACAICGAGAAGGAIGCCGCGCTGGAGGCGCTTCCAGAAG 1945
Qy	319	lyPheGlyValMetThrGlu-GluGluLeuLysLeuAlaValAlaAlaAlaArgLysArg 338
qq	1944	GTGCTGGTGGACGAACCGAGGAAGACACCATCGCCATCCTCCGTGGCCTCAAGGAA 1885
Οy	339	GlyGluLysValValMetThrAsnGlyValPheAspIleLeuHisAla 354
qq	1884	CGCIATGAAGTGCACCACGGGGTGAGCATCACCGACGGCGCGATCATCGCCGCG 1831
QY	355	GlyHisValSerTyrLeuAlaAsnAlaArgLysLeuGlyAspArgLeuIleVal 372
qq	1830	GCCAAGCTGTCGCACCGCTACATCACCGATCGGCAACTGCCCGACAAGGCCATCGAC 1774
Qy	373	AlaValAsnSerAspAlaSerThrLysArgLeuLysGlyAspSerArgProVal 390
QQ	1773	П
δλ	391	AsnProLeuGluGlnArgMetIleValLeuGlyAlaLeuGluAlaVal 406
qa	1713	GATCGTCTCGACCGTCGCCTGATCCAGCTGAAGATCGAGCGCCCAGGCGAAGAAGGAA 1654
Qy	407	pValValSerPheGluGluAspThrProGlnArgLeuIl@AlaGly
QQ	1653	GACGAGCCACCAGGAAGCGCCTGGCCAAG
Oy	427	yrLysProGluGluIle
QQ	1614	CTCGAGCGCGATACGCCGACCTCGAGGAGAT
Qy	447	lLeuAsnPheGluAspGlyCysS
QQ	1566	GGCTCGGCG 15
δy	466	AsnileileLysLysIleGinGinAspLysLys 476
qq	1530	CAGATCCAGCAGAAGATCGAGCAGCCAAGCAG 1498
RESU US-0 ; Se ; Pa	LT 13 9-221- quence tent N	ESULT 13 (S-09-221-017B-757 Sequence 757, Application US/09221017B Patent No. 6444799 GENERAL INFORMATION:

us-09-912-020-325.p2n.rni

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1026 GGCCCTTANGCCGCTGACGCTTTTTGGGGGTCGGATATGGCTCTGCATTTCGATGGCATT 1085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1287 GCATCGTGGCGATCGGCTACGCGCAATCCTCCGAAAGAGTTATTTCGAGCGGGCAAT 1346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1107 ATGTTTAAAGATAAAGACTATCGTTTACACATCCGGGACATTCGATATGTTCCACTACAAC 1466
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    83 SerLysSerLeuAlaAspvalAsnvalLysCysAspPhevalServalProThrHisPro 102
                                              ----CTGGTGACCATGCCGATCAACAA 665
                                                                                                                                    666 GCAGCCATGCCGCAGGACATCTTTCCATACAAAGGCCATACGGAATACCTGCAGGCCCAA 725
                                                                                                                                                                                                                                                                                                                                                        150 SerAspTyrAlaLysGlyAlaLeuAlaSerValGlnGlnMetIleGlnLeuAlaArgLys 169
                                                                                                                                                                                                                                                                                                                                                                                                    846 CTGGACAAGCTGAAGGCTTTCGATCGCAGCCTCCGCATGGATTTCGGTATAGTACGTCCG 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                170 AlaGlyValProValLeuIleAspProLysGlyThrAspPheGluArgTyrArgGlyAla 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 Glu---------------GluIleValGluArgGlyMetLysLeuIle 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 AspValThrGlyAlaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAlaAlaGly 277
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                                                                                        103 ThrIleThrLysLeuArgValLeuSerArgAsnGlnGlnLeuIleArgLeuAspPheGlu
                                                                                                                                                                                                                                                                    131 ---GlnProLeuHisGluArgIleAsnGlnAlaLeuSerSerIleGlyAlaLeuValLeu
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                                                                                                                                                                              123 GluGlyPheGluGlyValAspPro-----
                                              621 AAGCAAGCCGATGCGGATGTG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ROSS, Bruce C. TITLE OF INVELENTIBES AND USES THEREOF NUMBER OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3058
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72
211
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Mismatches:
Indels;
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27340-20021.00
                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEO for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/AU98/01023 FILING DATE: 10-DEC-1998 ATTORNEY/AGENT INFORMATION:
                                                                                        ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 2734
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                                                                                                      STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
AUGUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 706141
INFORMATION FOR SEQ ID NO: 757:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
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138.50
35.018
19.928
5.798
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FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 3058 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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LOCATION: 1...3058
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                                                                                                                                  CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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ORIGINAL SOURCE
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Best Local Similari
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25726 ---GACCCGAACGTCGAGGAGTCGCCCAGGCGCTGGACAAGTACACCGTCGACATGACC 25670
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                      25402 -------CTGAAGGCGGTCCTC-----AACGAACTGGGCAAG----- 25373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24940 GATCGTCCGACCGTCGCCTGATCCAGCTGAAGATCGAGCGCGAGGCGCTGAAGAAA 24881
                                                                                                                                                                                                                                                                                    163 MetileGlnLeu-----AlaArgLysAlaGlyValProValLeuIleAspProLysGly 180
                                                                                                                                                                                                                                                                                                                                                        181 ThrAspPheGluArgTyrArgGlyAlaThrLeuLeuThrProAsnLeuSer---- 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AlaValValGlyLysCysLysThrGluGluGluIleValGluArgGlyMetLysLeuIle 220
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                                                                    116 LeuIleArgLeuAspPheGlu------GluGiyPheGluGlyValAsp 129
                                                                                                                                          130 ProGlnProLeuHisGluArgIleAsnGlnAlaLeuSerSerIleGlyAlaLeuValLeu 149
                                                                                                                                                                                                               150 SerAspTyrAlaLysGlyAlaLeu-------AlaSerValGlnGln 162
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ValSerValProThrHisProThrIleThrLysLeuArgValLeuSerArgAsnGlnGln 115
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Db 457 ATAGCACANATCACCTGAAAAACTGGTGCGCAACTAGTTGTTGATGCAGAAAAGATCTTGTGTGTG				
	; TYPE: DNA ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-2746 Alignment Scores: 6.55e-06 Length: 939 Score: 137.50 Matches: 58 Percent Similarity: 43.28% Conservative: 58 Best Local Similarity: 21.64% Mismatches: 111 Query Match: 4.75% Indels: 12	US-09-912-020-325 (1-477) x US-09-134-001C-2746 (1-939) QY 51 GlyGlyalaAlaAsnvalalaMetasnIleAlaSerLeuGlyAlaAsnAlaArgLeuVal 70 11	Qy 91 ValLysCysAspPheValSerValProThrHisProThrIleThrLysLeuArgValLeu 110 11 11 11 SerArCAATTTTGTTCAAGTAGATGATGAGGATACGCGTATTAATGTAAAA 294 Qy 111 SerArgAsnGlnGlnLeuIleArgLeuAspPheGluGluGlyPheGluGlyValAspPro 130 1295 CTAAAATCAGGTCAAGAAACAGAAATCAATGCACCCGGACCT 336 Qy 131 GlnProLeuHsGluArgIleAsnGlnAlaLeuSerSerIle	Db 337 AAGTGACACGCGCATTTGACTTTATCTCATACGTCGTACTACAAACGAC 396 Qy 145 GlyAlaLeuSerAspTyrAlaLysGlyAlaLeuAlaSerValGlnGln 162 Db 397 GATATTGTAGTGGAAGTGTACCGAACAGTATTCCAAGTGCTTATGCACA 456 Qy 163 MetleGlnLeuAlaArgLysAlaGlyValProValLeuIleAspFrcLysGlyThrAsp 182

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Searched:

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7981, Ap
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Sequence 6279, Ap
Sequence 1264, Ap
Sequence 210, App
Sequence 9242, Ap
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6309, Ap
9788, Ap
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Fetent No. US2002022718A1
GENERAL INFORMATION:
APPLICANT: Forsyth, R. Allyn
APPLICANT: Ohlsen, Kari L.
APPLICANT: Oskind, Judith W.
TITLE OF INVENTION: Genes identified as required for TITLE OF INVENTION: BITTRA.009A
CURRENT APPLICATION UNMER: US/09/741,669
CURRENT APPLICATION NUMBER: US 60/173005
PRIOR APPLICATION NUMBER: US 60/173005
PRIOR PILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 481
SOFTWARE: FastSEQ for Windows Version 4:0
              US-09-815-242-6279
US-09-917-800A-1264
US-09-070-927A-210
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US-09-880-107-3376
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    TYPE: DNA ORGANISM: Escherichia coli
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LENGTH: 1434
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-Q-\cgn2_1/USPTQ_spool/US99912020/runat_25112002_091430_24365/app_query.fasta_1.647
-DEVEDLAD-APDITACTIONS_NA -QFMTA-fastap -SGFFIX-P2n.rnpb -MINMATCH=0.1
-LOOPEXT-0 -LOOPEXT-0 -UNITS-bits -START-1 -END--1 -MATRIX-blosum62
-TRR.MS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_PAX=100
-THR_MIN-0 -ALIGN-15 -MODE-LOCAL -QUTFMT-pto -NORM-ext +HEAPSIZE-500 -MINLEN-0
-MAXLEN-200000000 -USER-US0991202_0_@CGN_11_47_erunat_25112002_091430_24365
-NCPU-5 -NCPU-3 -NO_XLPXY -NO_MMAP -LARGDUERY -NG_SCORES-0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS-1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 165, App
Sequence 6204, Ap
Sequence 9661, Ap
                                                                                                  November 26, 2002, 22:04:38; Search time 113 Seconds (without alignments) 1625.664 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
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9: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
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              GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                         nucleic search, using frame_plus_p2n model
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US-09-912-020-165
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US-09-815-242-9661
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Listing first 45 summaries
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seq length: 2000000000
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Database :

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Matches 1393.00 Matches 477	DD 1 ATGAAAGTAACGCTGCCAGAGTTTGAACGTGCAGGAGTGATGGTGGTTGGT	41 VallysvalAsnThrIleGluGluArgProGlyGlyAlaAlaAsnValAlaMetAsnIle 60		Oy 101 HisbrothrileThrLysLeuargValLeuSerargAsnGlnGlnLeuileArgLeuAsp 120 	Oy 121 PheGluGluGluGlyPheGluGlyValAspProGlnProLeuHisGluArgIleAsnGlnAla 140 	Oy 141 LeuSerSerIleGlyAlaLeuValLeuSerÅspTyrAlaLysGlyAlaLeuAlaSerVal 160 	Oy 161 GlnGlnMetileGlnLeuAlaArgLySAlaGlyValProValLeuIleAspProLySGly 180	Oy 181 ThraspPheGluargTyrArgGlyAlaThrLeuLeuThrProAsnLeuSerGluPheGlu 200 	Oy 201 AlavalvalGlyLysCysLysThrGluGluGluIlevalGluArgGlyMetLysLeuIle 220 	Qy 221 AlaAspTyrGluLeuSerAlaLeuValThrArgSerGluGlnGlyMetSerLeuLeu 240 	Qy 241 GinproGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspValThr 260 	Oy 261 GlyAlaGlyAspThrValileGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeu 280 	Oy 281 GluGluAlaCysPhePheAlaAsnAlaAlaGlyValValValGlyLysLeuGlyThr 300 	Oy 301 SerThrvalSerProlleGluLeuGluAsnAlaValArgGlyArgAlaAspThrGlyPhe 320

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Conservative:
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BER: 09/492,709
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                                                                                                                                                                                                                                                 APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Yeal, Judith W.
APPLICANT: Yeal, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Wall, Boward
TITLE OF INVENTION: Identification of E.
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICANTION NUMBER: US/09/815,2
CURRENT APPLICATION NUMBER: 60/101,078
PRIOR APPLICATION NUMBER: 60/204,848
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/206,948
PRIOR FILING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                       Sequence 6204, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
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ORGANISM: Escherichia
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Best Local Similarity:
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US-09-815-242-6204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
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LENGTH: 1434
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Conservative::
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TTLE OF INVENTION: Identification of Essential Gen
TTLE OF INVENTION: Identification of Essential Gen
TTLE OF INVENTION: Identification of Essential Gen
TTLE OF INVENTION: Prockaryotes
USERIENT PELITRA, 011A
USRENT APPLICATION NUMBER: 00/103-21
RIOR APPLICATION NUMBER: 60/206, 848
RIOR FILING DATE: 2000-05-23
RIOR APPLICATION NUMBER: 60/207, 727
RIOR APPLICATION NUMBER: 60/207, 727
RIOR PELLING DATE: 2000-10-23
RIOR PELLING DATE: 2000-10-23
RIOR PELLING DATE: 2000-11-27
RIOR APPLICATION NUMBER: 60/257, 931
RIOR PELLING DATE: 2000-11-22
RIOR APPLICATION NUMBER: 60/257, 931
RIOR APPLICATION NUMBER: 60/269, 308
RIOR FILING DATE: 2001-10-216
DYWBER OF SEO ID NOS: 14110
DYWBER OF SEO ID NOS: 14110
SIND 9661
LENGTH: 1434
RYPE: DNA
SEAURE: SCALING: SCALING
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ent No. US20020061569A1
ENAL INFORMATION:
PLICANT: Haselbeck, Robert
PLICANT: Ollsen, Kari L.
PLICANT: Ollsen, Kari L.
PLICANT: Wall, Daniel
PLICANT: Wall, Daniel
PLICANT: Tawick, John D.
PLICANT: Yamancto, Robert T.
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ATION: (1)...(1434)
15-242-9661
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Query Match:
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                                                                                                                                           41 ValLysValAsnThrileGluGluArgProGlyGlyAlaAlaAsnValAlaMetAsnIle
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                                              US-09-912-020-325 (1-477) x US-09-815-242-7981 (1-1425)
  Conservative:
Mismatches:
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APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
TITLE OF INVENTION: Identification of Essenti
TITLE OF INVENTION: Deckaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 05/09/815,242
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/205,57
PRIOR APPLICATION NUMBER: 60/255
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE FRAEESO FOR WINDOWS Version 4.0
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Sequence 7757, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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Zyskind, Judith W.
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US-09-815-242-7757
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LENGTH: 927
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Alignment Scores: 5.67e-13 Length: 927 Fred. No.: 5.67e-13 Length: 927 Score: 197.00 Matches: 86 Percent Similarity: 41.85% Cónservative: 50 Best Local Similarity: 26.46% Mismatches: 153 Query Match: 10 Gaps: 11	US-09-912-020-325 (1-477) x US-09-815-242-7757 (1-927)	<pre>Qy 10 ArgAlaGlyValMetValValGlyAspValMetLeuAspArgTyrTrpTyrGlyProThr 29</pre>	Oy 30SerArglieSerProGluAlaProValProValValLysValAsn 44 :::::::::::::::::::::::::::::::::::	45 ThrileGluGluArgProGlyGlyAlaAlaAsnValAlaMetAsnIleAlaSerLeu	Oy 64 GlyAlaAsnAlaArgLeuValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLeuSer 83	<pre>Qy 84 LysSerLeualaAspValAsnValLysCysAspPheValSerValProThrHisPro 102</pre>	<pre>Qy 103 ThrileThrLysLeuargValLeuSerargAsnGlnGlnLeuIleArgLeuAspPheGlu 122</pre>	<pre>Qy 123 GluGlyPheGluGlyValAspProGlnProLeuHisGluArglleAsnGlnAla 140</pre>	Qy 141 LeuSerSerIleGlyAlaLeuValLeuSerAspTyrAlaLysGlyAlaLeuAlaSerVal 160 	Oy 161 GlnGlnMetIleGlnLeunlaArgLysalaGlyVaIProValLeuIleAspPro 178	Oy 179LysGlyThrAspPheGluArgTyrArgGlyAlaThrLeuLeuThrProAsnLeu 196 	<pre>Qy 197 SerGluPheGluAlavalValGlyLysCysLysThrGluGluGluGluLleValGlu 214</pre>	<pre>Qy 215argGlyMetLysLeuIlealaAspTyrGluLeuSerAlaLeuLeuValThrargSer 233</pre>	Qy 234 GluGlnGlyMetSerLeuLeuGlnProGlyLysAlaProLeuHisMetProThrGlnAla 253	254 GlnGluValTyrAspValThrClyAlaGlyAspThrValIleGlyValLeuAlaAlaThr	Db 730 GTCAAGGCGCTGGATACCACGGCGGCGACACCTTCGTCGGCGGGTTCGCCGCGGC 789	274 LeuAlaalaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnAlaAlaGlyVal 29	790 CTTGCGCGCGCGCCTCGACGAGGCGGCGGTCCGCTTCGGCCAGGCCGCCGCGGCGATC	OY 294 VALVAIGLYLYSELOUGIYTHENSETTHENTALSEPPETILEGLULGUGLUASHALA 311

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AAA---GAAATGCCAAAACCAGGCGAAACAATTCACGCCATTGAACATTTACAGCGGGT 117
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                                                                                                                                                                    PLICANT: Hase-beck, Robert
PLICANT: Hase-beck, Rari L.
PLICANT: Ohlsen, Kari L.
PLICANT: Ohlsen, Kari L.
PLICANT: Ohlsen, Kari L.
PLICANT: Tayind, Judith W.
PLICANT: Travick, John D.
PLICANT: Travick, John D.
PLICANT: Travick, John D.
PLICANT: Yamanorto, Robert T.
PLICANT: Yamanorto, Robert T.
PLICANT: Yamanorto, Robert T.
PLICANT: Au, H. Howard
T.E OF INVENTION: Identification of Essential Genes in
TLE OF INVENTION: Defortification of Essential Genes in
TLE OF INVENTION: Prokaryotes
LE REFERENCE: ELITRA.011A
RREW APPLICATION NUMBER: 60/191,078
IOR PILLING DATE: 2000-03-21
IOR PPLICATION NUMBER: 60/207,727
IOR APPLICATION NUMBER: 60/207,727
IOR APPLICATION NUMBER: 60/207,727
IOR APPLICATION NUMBER: 60/207,727
IOR APPLICATION NUMBER: 60/253,625
IOR FILING DATE: 2000-10-23
IOR PPLICATION NUMBER: 60/257,931
IOR PPLICATION NUMBER: 60/257,931
IOR PPLICATION NUMBER: 60/269,308
IOR FILING DATE: 2001-127
IOR APPLICATION NUMBER: 60/269,308
IOR FILING DATE: 2001-02-16
RABER OF SEQ ID NOS: 14110
FIRMARE: FastSEQ for Windows Version 4.0
FUNDAR: 918
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No. US20020061569Al
INFORMATION:
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TION: (1)...(918)
5-242-6795
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FILING DATE: 04-May-2000 CLASSIFICATION: CURROWN> PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/046,655 FILING DATE: 1997-05-16 APPLICATION NUMBER: 60/044,031 FILING DATE: 1997-05-06 APPLICATION NUMBER: 60/066,009 FILING DATE: 1997-11-14 ATTORNEY/AGENT INFORMATION: NAME: Kenley K. HOG-ver REGISTRATION NUMBER: 40,302 REFERENCE/DOCKET NUMBER: PB369 TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504 TELEPHONE: (301) 309-8512 INFORMATION FOR SEQ ID NO: 532: SEQUENCE CHARACTERISTICS: LENGTH: 1283 base pairs TYPE: nucled cacid STRANDEDNESS: double TOPOLOGY: linear SEGURNE DESCRIPTION: SEQ ID NO: 532: US-09-070-927A-532	1283 1283 1283 1283 1283 1285	Db 332GGGGGAAAAGGATTAAATCAAGCTGTGGCTTAACCAAACTGGGCCAT 379 Oy 66 AsnalaArgLeuValGlyLeuThrGlylleAspAspAlaArgAlaLeuSerLysSer 85
98 AspValAsnValLysCysAspPheValSerValProThrHisProThrIleThrLysLeu 107 111 11 11 11 11 11 11 1	195 ASNLeuSerGluPheGluAlaValValGlyLySCYSLySTHrGluGluG	Oy 294 ValvalGityFaleuGiyThtSerThrValSerProTileGiuLeuGiu 309

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GAAACATATTTATTGGGGTGTGTGGGAAATGCCGCTGGAGCTATGATGATTA 6760
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Conservative:
Mismatches:
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                                                        ID NO:
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ
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182.50
41.09%
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Best Local Similarity:
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                                                                                                                                  No.:
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APPLICANT: Charles A. Lillon
Statick J. Dillon
States
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ADDERSE: 982
CORRESPONDENCE ADDERSS:
ADDERSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                    955
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 AAACCAGCTGCTATTCATCATATTCCAGTGAATATACTAGAAAAGGTTGATTTT----- 760
                                                                                                                                                                                      AspTyrGluLeuSerAlaLeuLeuValThrArgSerGluGlnGlyMetSerLeuLeuGln 241
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                                                                                                                                                                                                                                                              242 ProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspValThrGly 261
                                      TyrArgGlyAlaThrLeuLeuThrProAsnLeuSerGluPheGluAlaValGlyLys
                                                                      -----TTCATTCCCAATGAAGATGAATTATTGGAACTTCAACCAGAT
                                                                                                            CysLysThrGluGluGlu------IleValGluArgGlyMetLysLeuIleAla
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb sto
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: CURNOWN>
PRIOR APPLICATION CURNOWN>
PRIOR APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORIEY AGENT INFORMATION:
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REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
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TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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COUNTRY: USA
ZIP: 20850
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US-09-912-020-325 (1-477) x US-09-974-300-839 (1-888)
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|92 TCATTACGGGAAAGCCATCCTCGACAATTTTCAAGCCAATGGTGTCTTGACAGACTATGT
                                               LeuGluAsnAlaValArgGlyArgAlaAspThrGlyPheGlyValMetThrGluGluGlu
                                                                                                           LeuLysLeuAlaValAlaAlaAlaArgLysArgGlyGluLysValValMetThrAsnGly
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                                                                                                                                                                                                                                                                                                        GENERAL INCOMMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
SPIOR FILING DATE: 2001-03-27
NUMBER OF SEX ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 747
LENGTH: 880
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Mismatches:
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Matches:
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Best Local Similarity:
Query Match:
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---GlyAlaLeuValLeu----
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Sequence 839, Application US/09974300
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Sequence 839, Application US/099974300
Sequence 839, Application US/09999974300
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Sequence 839, Application US/09999974300
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PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: 888
133 uHisGluArgIleAsnGlnAlaLeuSerSerIle---
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                                                                                   138 AGCGGTAGCCGCGCCCGGCTTGGCGCCCGAGGTCCATATGATCGGCTGCGTCGGCGATGA 197
                                                                                                                                                                                                                        198 TCATTACGGGAAAGCCATCCTCGACAATTTTCAAGCCAATGGTGTCTTGACAGACTATGT 257
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 MetLeuAspArgTyrTrpTyrGlyProThrSerArg-IleSerProGluAlaProVal-- 38
                  76 pAspAlaAlaArgAlaLeuSerLysSerLeuAlaAspValAsnValLysCysAspPheVa
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                                                             39 ----ProvalvalLysvalAsnThrIleGluGluArgProGlyGly---AlaAlaAsnVa
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Patent No. US20020061569A1
GENERAL INFORMATION:
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Zyskind, Judith W.
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W
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APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TILE OF INVENTION: Identification of Essential Genes in
TILE OF INVENTION: Prokaryous
FILE REPERENCE: ELITRA.011A
CURRENT FALING DATE: 2001-03-21
PRIOR PELICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-05-23
PRIOR PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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US-09-815-242-6938
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Best Local Similarity:
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LENGTH: 921
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                                                                                                                                                                                                                                                 239 LeuLeuGlnProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAsp 258
                                                                                                                                                                                                                                                                                                                                  ---GlnLeuAlaArgLysAlaGlyValProValLeuIleAspProLysGlyThr 181
                                                                        182 AspPhe-----GluArgTyrArgGlyAlaThrLeuLeuThrProAsnLeuSerGlu 198
                                                                                                                                                                                                                                                                                                                                                                                                         742 ACTACCGCAGCTGGTGATACATTTAATGGCGGTTTTGTTACGGCTTTATTGGAAGAAAA 801
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                                    445 CTGGCTGCTCAAATCGCTAAGAAAATGGTGTCAAGGTTGTGCTAAATCCTGCTCCAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                              SerLeuGluGluAlaCysPhePheAlaAsnAlaAlaAlaGlyValValValGlyLysLeu
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
TITLE OF INVENTION: Genes identified as required for TITLE OF INVENTION: proliferation of E. coli
FILE REFERENCE: ELITRA 009A
CURRENT FILING DATE: 2000-12-19
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 481
SOFTWARE: FastSEQ for Windows Version 4.0
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Mismatches:
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Patent No. US20020022718A1
GENERAL INFORMATION:
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Best Local Similarity:
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; LOCATION: (1)
US-09-741-669-286
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GTTGCATTTGGCGGCAAAGGCGCGAATCAGGCTGTGGCTGCTGGGCGTAGCGGTGCGAAT 171
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670 TTAGGAAGTCGTGGTGTATGGCTAGCGTGAATGGTGAAGGTCAG----CGCGTTCCTGGA
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                                                                       GluArgProGlyGly---AlaAlaAsnValAlaMetAsnIleAlaSerLeuGlyAlaAsn
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TITLE OF INVENTION: Identification of Essential Genes in
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APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
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Zyskind, Judith W.
Wall, Daniel
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-27
PRIOR PLING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-2
PRIOR FILING DATE: 2000-12-2
PRIOR FILING DATE: 2000-12-2
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASSESE FOR WINDOWS VERSION 4.0
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; LOCATION: (1)...(930)
US-09-815-242-6309
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Best Local Similarity:
Query Match:
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510 GATGCAGCGAGGGGCGCCAGGTACTGCATGAAAAGGTATCCGTACTGTACTGATACT 669
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                                                                                                               175 LeuIleAspPro-----LysGlyThrAspPheGluArgTyrArgGlyAlaThrLeu 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 IleValGluArgGlyMetLysLeuIleAlaAspTyrGluLeuSerAlaLeuLeuValThr 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 ArgSerGluGlnGlyMetSerLeuLeuGlnProGlyLysAlaProLeuHisMetProThr 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 GlnAlaGlnGluValTyrAspValThrGlyAlaGlyAspThrVallieGlyValLeuAla 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        272 AlaThrLeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnAlaAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuThrPrcAsnLeuSerGluPheGluAlaValValGlyLysCysLysThrGluGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           670 TTAGGAAGTCGTGTGTATGGCTAGCGTGAATGGTGAAGGTCAG---CGCGTTCCTGGA
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TITLE OF INVENTION: Identification of Essential Generative of INVENTION: Prokaryotes
TITLE OF INVENTION: DADIAGRATYOTES
CURRENT PAPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR PRILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
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PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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Patent No. US20020061563A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 14110
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; LOCATION: (1)...(933)
US-09-815-242-9878
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Search completed: November 27, 2002, 02:57:12 Job time : 130 secs 29: /cqn2_6/ptodata/2/pna/US097B_COMB.seq:*

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

    nucleic search, using frame_plus_p2n model

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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result

Description Sequence 6204, Sequence 276, Sequence 6204, Sequence 6204,	
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	(-09-912-020-325 (1-477) x PCT-US02-03987-6204 (1-1434)	1 MetLysva	1 ATGAAAGTAACGCTGCCAGAGTTTGAACGTGCAGGAGTGATGGTGGTTGGT	21 LeuAspArgTyrTrpTyrGlyProThrSerArglleSerProGluAlaProValProV	61 CTGGATCGTTACTGGTACGGCCCCACCAGTCGTATCTCGCCGGAAGCGCCGGTGCCCGTG	41 ValLysValAsnThrIleGluGluArgProGlyGlyAlaAlaAsnValAlaMetAsnIle 60	121 GTTAAAGTGAATACCATCGAAGAACGTCCGGGCGCGCGCG	61 AlaSerLeuGlyAlaAsnAlaArgLeuValGlÿLeuThrGlyIleAspAspAlaArg 80	181 GCTTCTCTCGGTGCTAATGCACGCCTGGTCGGGTTGACGGGCATTGACGATGCAGGGGG	81 AlaLeuSerLysSerLeuAlaAspValAsnValLysCysAspPheValSerValProThr 100	241 GCGCTGAGTAAATCTCTGGCCGACGTCAAATGCGAATTGCGTTTCTGTACCGAC	101 HisProThrIleThrLysLeuArgValLeuSerArgAsnGlnGlnLeulleArgLeuA	301 CATCCGACCATACCAAATTACGGGTACTTTCCCGCAACCAAC	121 PheGluGluGlvPheGluGlvValAspProGluProLeuHisGluArglleAsnGlnAla 14		301 IIIGAAGAAGGIIICGAAGGIGIIGAICCGCAGCGCACGAGCGGAGIIAAICAGGCG 42	141 LeuSerSerIleGlyAlaLeuValLeuSerAspTyrAlaLysGlyAlaLeuAlaS	421 CTGAGTTCGATTGGCGCGCTGGTTTCTGACTACGCCAAAGGTGCGCTGGCAAGCGT	161	481 CAGCAGATGATCCAACTGGCGCGTAAAGCGGGTGTTCCGGTGCTGATTCATCCAAAAGG	181 ThrAspPheGluArgTyrArgGlyAlaThrLeuLeuThrProAsnLe	541 ACCGATTTTGAGCGCTACCGCGGCGCTACGCTGTTAACGCCGAATCTCTCGGAATTTGA	201 AlaValValGlyLysCysLysThrGluGluGluIleValGluArgGl	601 GCTGTTGTCGGTAAATGTAAGACCGAAGAGATTGTTGAGCGCGCGC	221 AlaAspTyrGluLeuSerAlaLeuLeuValThrArgSerGluGlnGl	661 GCCGATTACGAACTCTCGGCTCTGTTAGTGACCCGTTCCGAACAGGGTATGTCGCTG 720	241 GlnProG	721 CAACCGGGTAAAGCGCCGCTGCATATGCCAACCCAAGCGCAGGAAGTGTATGACGTTACC 780	261 GlyAlaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsr		281 GluGluAlaCysPhePheAlaAsnAlaAlaAlaGlvValValValGlvLvsLeu		, 000000000000000000000000000000000000	301.SerThrValSerProIleGluLeuGluAsnAlaValArgGlyArgAlaAspThrGlyPhe 32	901 TCCACGGTTTCGCCGATCGAGCTGGAAATGCTGTACGTGGACGTGCAGATACAGGCTTT 96	321 GlyValMetThrGluGluGluLeuLySLeuAlaValAlaAlaAlaArgLySArgGlyGlu 340	961 GCCGTGATGACCGAAGAGGAACTGAAGCTGGCCGTAGCGGCGGGGCGGTAACGTGGTGAA 10	7 341 LysvalValMetThrAsnGlyValPheAspIleLeuHisAlaGlyHisValSetTyrLeu 360
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•	US-09-252-691-3421 US-09-252-691C-3421 DCT-1502-03087-9661	US-09-815-242-9661 US-10-072-851-9661	US-09-489-039A-2037 US-09-543-681A-2462	US-09-897-516-1461 US-09-897-516-1462	US-09-897-516-1463 US-09-897-516-1464	US-09-897-516-1465 US-09-897-516-1466	US-09-897-516-1467 US-09-897-516-1468	US-09-897-516-1469 US-09-897-516-1470	US-09-897-516-1471 US-09-897-516-1472	US-09-897-516-1473	US-09-897-516-3226	US-09-897-516-3228 US-09-897-516-3228	US-09-897-516-3229 US-09-897-516-3230	US-09-897-516-3231 US-09-897-516-3232	US-09-897-516-3233	US-09-897-516-3235	US-09-897-516-3236 US-60-215-161-1461	US-60-215-161-1462	US-60-215-101-1464	US-60-213-161-1463 US-60-215-161-1466 US-60-215-161-1467		ALIGNMENTS		S0203987	ENERAL INFORMATION: APPLICANT: Elitra Pharmaceuticals, Inc.	Identifying the Target ion	CURRENT APPLICATION NUMBER: PCT/US02/03987	7,636		ersion 4.0							Conservative: Mismatches:	Indels: Gaps:
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                           AlaLeuSerLysSerLeuAlaAspValAsnValLysCysAspPheValSerValProThr
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US-09-422-709A-165
US-09-422-709A-165
Sequence 165, Application US/09492709A
GENERAL INFORMATION:
APPLICANT: Cyskind, Judith
APPLICANT: Chisen, kari L.
APPLICANT: Foresth, R. Allyn
APPLICANT: Froelich, Jamie M.
APPLICANT: Froelich, Jamie M.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Wamamoto, Robert T.
APPLICANT: Waward
TITLE OF INVENTION: ESCHERICHIA COLI
TITLE OF INVENTION: ESCHERICHIA COLI
FILE REFERENCE: ELITRA, O01A
CURRENT APPLICANT: BLITRA, O01A
CURRENT APPLICAND NUMBER: US/09/492,709A
CURRENT APPLICAND NUMBER: US/09/492,709A
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 165
LENCE: DANA
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US-09-492-709A-165
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E. coli
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Mismatches:
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Matches:
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APPLICANT: Oblsen, Kari L.
APPLICANT: Oblsen, Kari L.
APPLICANT: Osykh, Kari L.
APPLICANT: Syskind, Judith W.
TITLE OF INVENTION: Genes identified as req
TITLE OF INVENTION: proliferation of E. col
FILE REFERENCE: ELITRA.009A
CURRENT APPLICATION NUMBER: US 60/173005
PRIOR FILING DATE: 1099-12-13
NUMBER OF SEQ ID NOS: 481
SOFTWARE: FastsEQ for Windows Version 4.0
SERIOTH: 1434
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Sequence 276, Application US/09741669
GENERAL INFORMATION:
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Best Local Similarity:
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US-09-741-669-276
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LeuSerSerIleGlyAlaLeuValLeuSerAspTyrAlaLysGlyAlaLeuAlaSerVal
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US-09-815-242-6204
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        AlaValValGlyLysCysLysThrGluGluGluIleValGluArgClyMetLysLeuIle
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Mismatches:
Indels:
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APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Osyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Travick, John D.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essenti
TITLE OF INVENTION: Identification of Essenti
TITLE OF INVENTION: Prokaryotes
FILE OF INVENTION: DADIE: 2001-03-21
FRIOR PRICK APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 6204
LENGTH:: 1434
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Matches:
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ORGANISM: Escherichia coli
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Best Local Similarity:
Query Match:
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US-09-815-242-6204
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Sequence 165, Application US/09912020
GENERAL INFORMATION:
APPLICANT: Oyskind, Judith
APPLICANT: Oyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Frostich, Railyn
APPLICANT: Frostich, Jamie M.
APPLICANT: Carr, Grant J.
APPLICANT: Tammoto, Robert T.
APPLICANT: Yamamoto, Robert T.
CURRENT EINKENTON: ESCHERICHIA COLI
FILE REFERENCE: ELITRA.001DV1
CURRENT APPLICATION NUMBER: 09/492,709
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 485
SOFTWARE: FastSEQ for Windows Version 3.0
BEOTO ID NO 165
BENTAL IN 1434
BENTAL IN 1434
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Matches:
Conservative:
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Indels:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
APPLICANT: Fu, H. Howard
APPLICANT: Fundise, J. Gordon
APPLICANT: Zamudio, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Olsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
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             SerThrValSerProIleGluLeuGluAsnAlaValArqGlyArqAlaAspThrGlyPhe
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GENERAL INFORMATION:
APPLICANT: Keith G. Weinstock et al.
TITLE OF INVENTION: UGCLEIC ACID AND AMINO ACID SEO(
TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THEIR
FILE REPERENCE: 107196-135
CURRENT APPLICATION NUMBER: US/09/252,691B
CURRENT FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 11324
SEQ ID NO 3421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Enterobacter cloacae US-09-252-691-3421
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APPLICANT: Yamamoto, Robert T.

APPLICANT: Roemer, Terry
APPLICANT: Roemer, Terry
APPLICANT: Janaq, Bo
APPLICANT: Boone, Charles
APPLICANT: Bussey, Howard
TITLE OF INVENTION: Wethods for Identifying the Target of a Compound which Inhibits of INVENTION: Proliferation
FILE REFERENCE: ELITRA.028A
CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6204
LENTH: 1434
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Matches:
Conservative:
Mismatches:
Indels:
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NAME/KEY: CDS

LOCATION: (1)...(1434)

US-10-072-851-6204
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Best Local Similarity:
Query Match:
DB:
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Length: Matches: Conservative: Mismatches: Indels:	2-691-3421 (1-1449	uArgAlaGlyValMetValV - - - - - - - - - - - - - - - - - - -	rgIleSerProG 	gProGlyGlyAlaalaAsr TCCCGTGCCCGCAAAC	uValGlyLeuThrGlylle 	AsnvallysCysAspP 	LeuSerArg }	pProGlnProLeuHisGluArg ::: TCCCGAGCCGCTGCACGAGCGC	SerAspT 	gLysAlaGlyValProValLeulle caaaGCCaGCGTTCCGGTGCTGATC	GlyAlaThrLeuLeuThrProAsnLeuSerG 	SCYSLYSThrGluGluGluIleValGluArgG 	eralaLeuLeuValThrArgSerGluG] 	sAlaProLeuHisMetProThrGlnAlaGlnGluVal' 	yvalLeualaalaThrLeualaal. 	laAsnAlaAlaAlaG]yValValVa 	IGLUASNA LAVA LAYGGLYAF.
3.1e-196 2299.00 98.95% : 94.96% 16.07%	477) x US-09-25	rrLeuProGluPheGluArgAl 	YrTrpTyrGlyProThrSerA 	nThrileGluGluArgE:	/AlaAsnAlaArgLe :::::: GCACATTCGCGTCT	rLeuAlaAspVa 	ThrLysLeuArgVa 	yPheGluGlyValAspi GTTCGAAGGCGTTGAT	eGlyAlaLeuValLe 	nMetIleGlnLeuAlaArgLy. 	Tyrarg Tarcgc	yLysCysLysThrGlu 	GluteuSerAlaLeuLe: 	rsalaProLeuHisMe: 	ThrvalileGl	sPhePheal:::	rProlleGluLer :GCCAATTGAGCTG
Scores: : :imilarity: : Similarity ch:	-020-325 (1-	MetLysvalThrLeu 	LeuAspArgT CTGGATCGCT	ValLysValAsı 	AlaSerLeuGl	AlaLeuSerLysSe	HisProThril	PheGluGluGly IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	LeuSerSerIle	GlnGl 	ThraspPheGluarg	AlavalvalGlyLys	AlaAspTy1 ::: GCTGATTTC	GlnProGlyLy:	GlyalaGlyAsp1 	GluGluAlaCy 	SerThrValS CCACCGTTT
Alignment Pred. No. Score: Percent S Best Loca Query Math	18-09-912	Oy 1 Db 19	2y 21 ob 79	Qy 41 Db 139	2y 61 Db 199	2y 81 0b 259	2y 101 0b 319	2y 121 bb 379	2y 141 0b 439	2y 161 Db 499	2y 181 ob 559	2y 201 ob 619	2y 221 0b 679	2y 241 0b 739	2y 261 pb 799	2y 281 Db 859	Oy 301 Db 919
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RESULT 8

US-09-252-691C-3421
; Sequence 3421. Application US/09252691C
; GENERAL INFORMATION:
    APPLICANT: Keith G. Weinstock et al.
    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTE
; TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: US/09/252,691C
; CURRENT APPLICATION NUMBER: US/09/252,691C
; CURRENT FILING DATE: 1999-02-18
; PRIOR PELLING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 11326
; SEQ ID NO 3421
; LENGTH: LA49
                                         1099 GCGAATGCGCGCAAGCTGGGCGACCGCCTGATTGTGGCGGGTCAACAGCGATGCCTCAACC 1158
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Matches:
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                                                                                        GlnProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspValThr
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           LeuSerSerIleGlyAlaLeuValLeuSerAspTyrAlaLysGlyAlaLeuAlaSerVal
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Matches:
Conservative:
Mismatches:
Indels:
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                                                  APPLICANT: MAIL, DAINEL
APPLICANT: Tradit, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essenti
TITLE OF INVENTION: Identification of Essenti
TITLE OF INVENTION: PROKATYOLES
TITLE OF INVENTION: PROKATYOLES
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR FILING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR FILING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/253,025
PRIOR APPLICATION NUMBER: 60/253,025
PRIOR APPLICATION NUMBER: 60/253,0308
PRIOR SEQ ID NOS: 14110
SOFTWARE: FASTERD FOR WINDOWS Version 4.0
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Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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US-09-815-242-9661
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Sequence 9661, Application US/09815242

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<u> </u>	141	; APPLICANI: ; APPLICANT: ; APPLICANT:
δ	GlnGlnMetIleGlnLeuAlaArgLysAlaGlyValProValLeuIleAspProLysGly	: APPLICANT:
QQ		; APPLICANT: ; APPLICANT:
Qy	181 ThraspPheGluArgTyrArgGlyAlaThrLeuLeuThrProAsnLeuSerGluPheGlu 200	; APPLICANT:
qq		; APPLICANT:
Οy	201 AlavalvalGlyLysCysLysThrGluGluGluIleValGluArgGlyMetLysLeuIle 220	; APPLICANT: ; APPLICANT:
QQ	601 GCGGTTGCGGGGAAATGTAAAAGCGAAGACGAACTGGTTGAACGCGGCATGAAGCTCATT 660	; TITLE OF INV
Qy	221 AlaAspTyrGluLeuSerAlaLeuLeuValThrArgserGluGlnGlyMetSerLeuLeu 240	; FILE REFEREN ; CURRENT APPL
qq	661 GCCGATTACGACCTTTCCGCGCTGTTGGTCACGCGTTCCGAACAGGGAATGACGCTGCTG 720	PRIOR APPLIC
οy	241 GlnProGlyLysalaproLeuHisMetProThrGlnAlaGlnGluValTyrAspValThr 260	, NUMBER OF SEC
qq	721 CAACCGAATAAAGCGCCGCTACATATGCCGACGCGCAGGCAG	
ολ	261 GlyalaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeu 280	TYPE: DNA
Q	781 GGTGGGGGGATACGGTGATCGGCGTGCTGGCGGCGGCGGGGGGAAATACCCTG 840	
yo d	281 GluGluAlaCysPhePheAlaAsnAlaAlaAlaAlyValValValGlybysLeuGlyThr 300 	S
3 8	GDT#hrValGarbrotleClifenGlubenalaValarnalabenalabenmente	Alignment Score
. d		Score: Percent Similar
ò	GlvValMotThrGluGluGluGluIveIoualaValalaalaardiveardCluGlu	Best Local Simi
5 A	GGCGTCATGACCGAAGAGGAGTTGAGACAGGCCGTCGCCAGCGCGCGTAAAGCGTGGCGG	DB:
ò	341 IvsValValWetThrasnGlvValDheasnTleLenHsAlaGlvHsValSerTvrLen 360	US-09-912-020-3
		Oy 1 MetLy
ò	AlaAsnAlaArqLvsLeuGlvAspArqLeuIleValAlaValAsnSerAspAlaSerThr	Db 1 ATGAA
8	GCGAACGCGCGCAAACTGGGCGACCGCCTGATTGTTGCGGGCCAATAGTGACGCCTCGACT	Qy 21 LeuAs
οy		61
Db 1		
ογ	401 GlyalaLeuGlualaValaspTrpValValSerPheGluGluAspThrProGlnArgLeu 420	121
Db 1	.201 GGGGGGTGGAGTGGGTTGTGTGTGTTTTGAAGAGGATAGGCGAAGAGAAGAAGAAGAAGAGAAGAGAAGAGAAGAGAAGA	OY OI AIASE
οy	IleAlaGlyIleLeuProAspLeuLeuValLysGlyGlyAspTyrLysProGluGluIle	81
Dp 1	ATTGCCGGTATTCTGCCGGATCTGCTGGTAAAAGGCGGCGACTATAAGCCGGAAGAGATC 1	Db 241 GCGCT
70 7	AlaGlySerLysGluValTrpAlaAsnGlyGlyGluValLeuValLeuAsnPheGluAsp	Oy 101 HisPro
a (Db 301 CATCC
7 B 6	401 GIYCYSSGTINTINIASDILELLELYSLYSILGGINGLAASPLYSLYS 476 	Oy 121 PheGl
RESULT 11		Db 361 TTTGA

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Bussey, Howard
WENDEDS Methods for Identifying the Target of a Compound which Inhibit
WENTION: Proliferation
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Conservative:
Mismatches:
Indels:
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                                                               Carr, Grant J.
Xu, H. Howard
Foulkes, J. Gordon
Samudo, Carlos
Haselbeck, Robert
Ohlsen, Kari L.
Cyskind, Judith W.
Wall, Daniel
Trawick, John D.
Yamamoto, Robert T.
Foemer, Terry
Jiang, Bo
Boone, Charles
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DB:
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; Sequence 2037, Application US/09489039A
; GENERAL INFORMATION:
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Gary Breton et.

APPLICANT:

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NN: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA NN: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS 2709.2004001
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Matches:
Conservative:
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TITLE OF INVENTION: NUCLEIC ACLD AND THE TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTIVE FILE REFERENCE: 2709.2004.001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
SQ ID NO 2037
THING DATE: 1999-01-29
SQ ID NO 2037
                                                                                                                                                                                                                                                              (1-477) x US-09-489-039A-2037
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2227.00
97.47%
92.19%
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                                                                                                                     TYPE: DNA
ORGANISM: Klebsiella
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Best Local Similarity:
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US-09-912-020-325 (1-477) x US-09-543-681A-2462 (1-1478)	Qy 1 MetlysvalThrLeubroGlupheGluargalaGlyvalMetvalvalGlyaspValMet 20	Qy 21 LeuAspArgTyrTrpTyrGlyProThrSerArgIleSerProGluAlaProValProVal 40 	Oy 41 VallysValAsnThrIleGluGluArgProGlyGlyAlaAlaAsnValAlaMetAsnIle 60 	Oy 61 AlaSerLeuGlyAlaAsnAlaArgLeuValGlyLeuThrGlyIleaspAspAlaArg 80	Qy 81 AlaLeuSerLysSerLeuAlaAspValAsnValLysCysAspPheValSerValProThr 100	QY 101 HisProThr1leThrlySLeuArgValLeuSerArgAsnGlnGhnLeuileArgLeuAsp 120	Oy 121 PheGluGluGluGlyPheGluGlyValaspFroGlnFroLeuHisGluargIleasnGlnAla 140	Oy 141 LeuserSerIleGlyAlaLeuValLeuSerAspTyrAlaLysGlyAlaLeuAlaSerVal 160 	Qy 161 GinGinMetileGinLeualaArgLysalaGiyValProValLeuileAspProLysGiy 180	Oy 181 ThrAspPheGluargTyrargGlyalaThrLeuLeuThrProAsnLeuSerGluPheGlu 200 :::	Oy 201 AlavalvalGlyLysCysLysThrGluGluIlevalGluArgGlyNetLysLeuile 220	Oy 221 AlaAspTyrGluLeuSerAlaLeuLeuValThrArgSerGluGlü3lyNetSerLeuLeu 240	Oy 241 GlnProGlyLysalabroLeudisMetProThrGlnalaGlnGluValTyraspValThr 260 1::	Oy 261 GlyAlaGlyAspThrValileGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeu 280	Qy 281 GluGluAlaCysPhePheAlaAsnAlaAlaGlyValValValVa: 31ytysLeuGlyThr 300 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 301 SerThrValSerProIleGluteuGluAsnAlaYalargGlyArgAlaAspThrGlyPhe 320	Qy 321 GlyValMetThrGluGluGluLeuLysLeuAlaValAlaAlaAlaArgLysArgGlyGlu 340	Oy 341 LysValValMetThrAsnGlyValPheAspIleLeuH1SAlaGlyHisValSerTyrLeu 360 :::::
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	AsnSerLeu 280 ::: ACACCCTG 906	leuGlyThr 300 	rhrGlyPhe 320 	argGlyGlu 340 GCGGCGAG 1086	SerTyrLeu 360 CCTATCTG 1146		lleValLeu 400 	31nArgLeu 420 	3luGluIle 440 ::: 3AGCAGATC 1386	pheGluAsp 460 TTGAAGAT 1446			RELATING TO PROTEUS MIRABI					
	GlyAlaGlyAspThrVallleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeu 	laalaalaGlyvalvalvalGlyLys 	luAsnalaValArgGlyArgAlaAsp' 	ysLeualavalalaalaalaargLys) 	heAspIleLeuHisAlaGlyHisVal: 	AlaAsnAlaArgLysLeuGlyAspArgLeuIleValAlaValAsnSerAspA. 	roValasnProLeuGluGlnargMet. 	Glyalaleuglualavalasptrpvalvalserpheglugluaspthrprog 		AlaGlySerLysGluValTrpAlaAsnGlyGlyGluValLeuValLeuValDeuSnPh 	ysLysIleGlnGlnAsp 474 GAAAATACAAAAGAT 1488	43681A	ACID SEQUENCES EUTICS	9/543,681A 128,706			Length: 1476 Matches: 389 Conservative: 43	Mismatches: 41 Indels: 0 Gaps: 0
	261 GlyAlaGlyAspthrValileGlyVa 	281 GluGlualacysPhePheAlaAsnAlaAlaAlaGlyValValValOJyLysLeuGlyThr 	301 SerThrValSerProIleGluLeuGluAsnAlaValArgGlyArgAlaAspThrGlyPhe	321 GlyvalmetThrGluGluGluLeuLysLeuAlavalAlaAlaAlaArgLysAl 	341 LysValValMetThrAsnGlyValPheAspIleLeuHisAlaGlyHisValSerTyrLeu 	361 AlaAsnAlaArgiysLeuGlyAspAr 	381 LysargLeuLysGlyaspSerargProValasnProLeuGluGlnargMetI: 	401 GlyalaLeuGlualaValaspTrpVa 	421 IlealaGlyIleLeuProAspLeuLe 	441 AlaGiySerLysGluValTrpAlaAs 	461 GlyCysSerThrThrAsn11elleLysLyslleGlnGlnAsp 474 	SULT 13 1-09-543-681A-2462 Sequence 2462, Application US/09543681A GENERAL INFORMATION	PLICANT: GARY BRETON FLE OF INVENTION: NUCLEIC ACID FLE OF INVENTION: DIAGNOSTICS E PERFEDENCE: 3700, 1003-001	CURRENT APPLICATION NUMBER: US/09/543,681A CURRENT FILING DATE: 2000-04-05 PRIOR APPLICATION NUMBER: US 60/128,706 PRIOR FILING DATE: 1090-04-09	MET 1476			best Local Similarity: 82.24% Query Match: 83.87% DB:
qa	Qy Dp	Qy	Qy Db	QY Db	Qy	δλ	oy Ob	Qy Dp	ογ Op	Oy Op	Oy Op	RESULT US-09-	AFF		SEO	, 0 ; 0S-09	Pred. No.: Score: Percent Si	DB:

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                        AlaAsnAlaArgLysLeuGlyAspArgLeuIleValAlaValAsnSerAspAlaSerThr
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Mismatches:
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Matches:
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APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Huesing, Joseph E.
APPLICANT: Krasonil-Osterfeld, Karina C.
APPLICANT: Malvar, Thomas M.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome Sc
FILE REFERENCE: 38-21(51847)B
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215, 161
PRIOR APPLICATION NUMBER: US 60/215, 161
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
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2.09-897-516-1461/c
Sequence 1461, Application US/09897516
GENERAL INFORMATION:
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; LOCATION: (877)...(1428)
US-09-897-516-1461
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Best Local Similarity:
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                IleAlaGlyIleLeuProAspLeuLeuValLysGlyGlyAspTyrLysProGluGluIle
                          Sequences And
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Matches:
Conservative:
Mismatches:
                                                                                    Sequence 1462/C
Sequence 1462, Application US/09897516
GENERAL INPORMATION:
APPLICANT: Corbin, David R.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Krasomil-Osterfeld, Karina C.
APPLICANT: Spiridonov, Sergei
APPLICANT: Spiridonov, Sergei
TILE OF INVENTION: Xenorhabdus sp. Genome Seq
FILE REFRENCE: 38-21(51847)B
CURRENT FILING DATE: 2001-06-29
PRIOR PPLICATION NUMBER: US/09/897,516
CURRENT FILING DATE: 2000-06
NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 1462
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ORGANISM: Xenorhabdus sp.
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; LOCATION: (1739)..(1870)
US-09-897-516-1462
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Best Local Similarity:
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09-897-516-1462/c
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                                   LeuSerSerIleGlyAlaLeuValLeuSerAspTyrAlaLysGlyAlaLeuAlaSerVal
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Search completed: November 27, 2002, 01:55:53. Job time : 3642 secs

Sequence 1809, Ap Sequence 100, App Sequence 45784, A Sequence 45791, A Sequence 27, App1 Sequence 45795, A Sequence 45795, A Sequence 45792, A Sequence 45793, A Sequence 45793, A Sequence 45793, A Sequence 18793, A Sequence 1877, A Sequence 18793, A P Sequence 18794, App1 Sequence 17794, A

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Searched:

Title: Perfect score:

Sequence:

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Scoring table:

Sequence

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APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTERCOCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 032796-032 CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/055,778 PRIOR APPLICATION UNBER: US 60/055,778 NUMBER OF SEQ ID NOS: 6812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   655 ATGATTGTAGTGGGTAGTTTAAACGTTGATAATTATCTGTATTCAACAAATTTACCACAT 714
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PCT-US02-32727-16

US-09-134-000C-1809

US-10-264-213-100

US-09-724-676-45781

US-09-724-676-45791

PCT-US02-32727-21

US-09-724-676-45794

US-09-724-676-45794

US-09-724-676-45794

US-09-724-676-45795

US-10-092-4114-1063

US-10-271-889-32

US-10-160-539A-19

PCT-US02-32727-41

PCT-US02-32727-41

US-09-134-000C-2275
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Mismatches:
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US-09-134-000C-1119
SG-09-134-000C-1119, Application US/09134000C
GENERAL INFORMATION:
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US-09-134-000C-1119
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    Percent Similarity:
Best Local Similarity:
      SEQ ID NO 1119
LENGTH: 1590
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-Q-cgn2_1/USPTO_spool/US09912020/runat_25112002_091430_24333/app_query.fasta_1.647
-Da-Bending_Pacents_NA_New -QFWT_stastap -SUFFX*=pro. rnpn - MINMATCH=0.1
-LOOPEXT=0 - LOOPEXT=0 - UNITS=bits - START=1 - END--1 - MATRIX=blosum62
-TRANS=human40.cdi - LIST=45 - DOCALIGN=200 - THR_SCORE=pct - THR_AMX=100
-THR_MIN=0 - ALIGN=15 - MODEL-COAL - OUTFWT*-pto - NORM-ext - HEAPSIZE=500 - MINLEN-0
-MAXLEN=200000000 - USER=US0991202_0_6GGN_1154_crunat_25112002_091430_24333
-NCPU=6 - NO_XLPXX - NO_MMAP - LARGEQUERY - NG_SCORES=0 - WAIT - LONGLOG
-DEV_TIMEOUT=120 - WARN_TIMEOUT=30 - THREADS=1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELDEXT=7
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Sequence 2723, Ap
Sequence 56, Appl
Sequence 107, Appl
Sequence 176, Appl
Sequence 176, Appl
Sequence 132, Appl
Sequence 1132, Appl
Sequence 1131, Appl
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                                                                                                                                               November 26, 2002, 21:16:58 ; Search time 112 Seconds (without alignments) 1876.398 Million cell updates/sec
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2393
1 MKVTLPEFERAGVMVVGDVM......FEDGCSTINIIKKIQQDKKG 477
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11. /cgn2_6/ptodata/2/pna/CT_NEW_COMB.seq:*

22. /cgn2_6/ptodata/2/pna/USO6_NEW_COMB.seq:*

33. /cgn2_6/ptodata/2/pna/USO7_NEW_COMB.seq:*

44. /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

55. /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

56. /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

77. /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*
                        GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd

    nucleic search, using frame_plus_p2n model

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US-10-092-411A-1684
US-10-092-411A-2723
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US-10-092-411A-2746
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1132 AAACCAGCTGCTATTCATCATATTCCAGTGAATATACTAGAAAAGGTTGATTTT----- 1185
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                                                                                                                                                                                               105
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                                                                                                                                                                                                                   -------GGCGGAAAAGGATTAAATCAAGCTGTTGGCTTAACCAAACTGGGCCAT
                                                                                                                        66 AsnAlaArgLeuValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLeuSerLysSer
                                                                                                                                                             CAGGCCACCTTAATTGGTTGTTTAGGCTCAGACACAGATGCGAATTACTTATAAAGAA
                                                                                                                                                                                               LeuAlaAspValAsnValLysCysAspPheValSerValProThrHisProThrIleThr
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                                                   46 IleGluGluArgProGlyGlyAlaAlaAsnValAlaMetAsnIleAlaSerLeuGlyAla
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APPLICANT: Havukkala, Ilkka J
APPLICANT: Lubbers, Mark William
APPLICANT: Debers, James APPLICANT: Debers, James TITLE OF INVENTION: Polynucleotides, materials incorporating TITLE OF INVENTION: them, and methods for using them.
1501 GATTCTTTAGTTGATCACGTCACTTTGGAAAAT 1533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---SerThrValSerProlleGluLeuGluAsn 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5280 AAGGGGCCAATCAAGCGGTTGCGGCGGCGATCTGGCGCTAAGACCAATTTCATCGGG 5221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5220 CGCGTCGGG---GATGATGCCAATGCTGCTTTCAGGCGTGGCGAGTTGGTGAAAAATCAA 5164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5163 ATTGATACCCAATATGTTGCGACCACGCCAGACACGGAAACCGGCCAGGCGTATATTCTG 5104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 AlaAspValAsnValLysCysAspPheValSerValProThrHisProThrIleThrLys 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 PheGluGlyValAspProGlnProLeuHisGluArgIleAsnGlnAlaLeuSerSerIle 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 GlyAlaLeuValLeuSerAspTyrAlaLysGlyAlaLeu------AlaSerVal 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 GlnGlnMetIleGlnLeuAlaArgLysAlaGlyValProValLeuIleAspProLysGly 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 ThraspPheGlu------ArgTyrArgGlyAlaThrLeuLeuThrProAsnLeu 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MetLysLeuIleAlaAspTyrGluLeuSerAlaLeuLeuValThrArgSerGluGlnGly 236
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74
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144
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Mismatches:
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                                                                                                                                                                                                                                   Length:
Matches:
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FILE REFERENCE: 11000.1043c3
CURRENT APPLICATION NUMBER: US/10/264,213
UGRRENT FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                  TYPE: DNA
; ORGANISM: Lactobacillus rhamnosus
US-10-264-213-15
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170.50
41.99%
23.72%
7.12%
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Best Local Similarity:
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                                                                                            SEQ ID NO 15
LENGTH: 7210
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PRIOR APPLICATION NUMBER: US 09/134,001 PRIOR PLILING DATE: 1999-08-13 PRIOR FILING DATE: 1997-08-13 PRIOR PELICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-08-14 PRIOR FILING DATE: 1997-08-14 NUMBER OF SEQ ID NOS: 5676 LENGTH: 948 TYPE: DNA ORGANISM: Staphylococcus epidermidis TYPE: DNA 1: ORGANISM: Staphylococcus epidermidis	a 6 a 6 a 6	631 AGTGATATGAAACAGCAACATATTTCTCGATTTAGGTATATCTCGAGTATTATAGTATTTTCACGATTTAGGTATATCTCCAGTATTAAATT 231 ThrargSerGluGlnGlyMetSerLeuLeuGlnProGlyLysAlaProLeuHisNetPro 1
Alignment Scores: 1.53e-06 Length; Score: 1.53e-06 Matches: 77 Matches: 77 Percent Similarity: 22.65\$ Mismatches: 142 Query Match: 6.92\$ Indels: 63ps: 13 US-09-912-020-325 (1-477) x US-10-092-411A-1684 (1-948)	DD QY DD RESULT US-10- Seque	808 TTARGIGAGTTARATARAGATTIGAGGARITTAGAATCGGCTATTGGAGTTGGAGTTGCAAATCAA 290 AlaalaGlyValValValGlyLysLeuGlyThrSerThrValSerFroIleGluLeuGlu 111:::::: 1 :::: 1 868 GCGTCGTCTCTAACGGTACAAAGGAGCACAAGCTTCTATACCAACACGTAAAGAA 1 4 -092-411A-2723 uence 2723, Application US/10092411A ERAL INFORMATION:
luPheGluArgAlaGlyValMetValValGlyAspValMetLeu	A TITI	APPLICANT: Lynn Doucette-Stamm et al APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: BPIDERALDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 032796-101 CURRENT FILING DATE: 2002-03-07 PRIOR APPLICATION NUMBER: US 09/134,001 PRIOR PLING DATE: 1998-08-13 PRIOR FILING DATE: 1998-08-13 PRIOR FILING DATE: 1997-08-14 PRIOR FILING DATE: 1997-08-14 NUMBER OF SEQ ID NOS: 5676 SEQ ID NO 2723 LENGRH: 414 TYPE: DNA TYPE: DNA ORGANISM: Staphylococcus epidermidis
235 AACTITATATTGGAA	Alignm Pred. Score: Percen: Best I Query DB: US-09-	Alignment Scores: 1.23e-05

STAPHYLOCOCC

48 GluArgProGlyGlyAlaalaAsnValAlaMetAsnIleAlaSerLeuGlyAlaAsn 48 GluArgProGlyGlyAlaalaAsnValAlaMetAsnIleAlaSerLeuGlyAlaAsn 48 GluArgProGlyGlyAlaalaAsnValAlaMetAsnIleAlaSerLeuGlyAlaAsn 48 GluArgProGlyGlyLeuThrGlyIleAspAspAlaAsnIleAlaSerLeuGlyAlaAsn 67 AlaArgLeuValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLeuSerLeu 572 CTGACCCCGGCGGTGGGGAGCTGAGCTGTGGCGTTCAG 67 AlaArgLeuValGlyLeuThrGlyIleAspAspAlaAshAshAshCGCCTATCCCTA 76 AlaAspValAsnValLySCYSASpPheValSerValProThrHisFroThrIleThrLyS 77 AlaAspValAsnValLySCYSASpPheValSerValProThrHisFroThrIleThrLyS 76 AlaAspValAsnValLySCYSASPPheValSerValProThrHisFroThrIleThrLyS 76 CTATCGGAAGGCGTTGGCCTTGAT	Oy 107 LeuargValLeuserArgAsnGlnGlnLeurlleArgLeuaspPheGlu 122 Db 2743 ACGGCCTCGTCGTCGCGGATTCCGGAGAACTCATTCTCTCTC	0 · 0 + -4 + 0 4 - 0	Oy 309 GluAsnAlaValArgGly
341 LysValValMetThrAsnGlyValPheAspIleLeuHisAlaGlyHisValSerTyrLeu 	Db 193 GAGTCTATTAGATACGTAGATTAGTTATCCCTGAAGAAGGACAGAAAGAA 249 Qy 421IlealaGlyIleLeuProAspLeuLeuValLysGlyGlyAspTyrLysProGlu 438 :::	: Zhang, Yanni : Wang, Siqing : Wang, Siqing : Jodes, Shyian : Lodes, Michael : Benson, Darin : Jones, Robert : Carter, Darrick : Barth, Brenda : Douglass, John : INVENTION: Compositions and Methods for the PPLICATION NUMBER: PCT/US02/32727 ILING DATE: 2002-10-11 SEQ ID NOS: 30992 5636 : Propioni acnes 27-56 ores:	

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TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne FILE REFERENCE: 210121.514c1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
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 13059 GTCGTGATGGTCACCCGAGTGGCCAACGATGTGTTCGCCGACACCA:GTTGGACAACTTT 13000
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12573 ATCATCGTAACTTTGGGCTCGCGTGGTGGGGCCCACGCAGAGGACGCAAAATC 12514
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                                                                                                             LysCysAspPheValSerValProThrHisProThrIleThrLysLeuArgValLeuSer 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 GlyAlaThrLeuLeuThrProAsnLeuSerGluPheGluAlaValValGlyLySCysLys 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 ArgAsnGlnGlnLeuIleArgLeuAspPheGluGluGlyPheGluGlyValAspProGln
                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuLeuVal?hrArgSerGluGlnGly...-MetSerLeuLeuGlnProGlyLysAlaPro
                                                                         12999 CGCAAAAACSGTATCGATACTACCCATGTTG---CGTACCGATGCSAGCTCCGGGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 ThrGluGluGluIleValGluArgGlyMetLysLeuIleAlaAspTyrGluLeuSerAla
                                      -- AspAlaAlaArgAlaLeuSerLysSerLeuAlaAspValAsnVal
                                                                                                                                                                                                                                                                                                                                   152 TyralaLysGlyalaLeuAlaSerValGlnGlnMetIleGlnLeuAlaArgLysAlaGly
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GENERAL INFORMATION:
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Zhang, Yanni
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Persing, David
Bhatia, Ajay
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Jen, Shyian
Lodes, Michael
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Barth, Brenda
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                                                                                                                                                                                  3540 GAGGTTTTCGACGCCATCCTCGACGAAGTGGTCGTGGACGGAGCCACGATTGCTCACGAG 3599
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3600 GCTCTCGGGCATGAACCGGAATCTTGGGTGAGAAACGGATTGAAGAGGTTCACACGGTC 3659
                         419 ArgLeuIleAlaGlyIleLeuProAspLeuLeuValLysGlyGlyAspTyrLysProGlu 438
LysGlyAspSerArgProValAsn------proLeuGluGlnArgMetIleValLeu 400
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                                                                         GlyAlaLeuGluAlaValAspTrpValValSerPheGluGluAspThrPro--
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Matches:
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Persing, David
Bhatia, Ajay
Maisonneuve, Jean Francois
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                                                                                                           3522 GGA-----
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Wang, Siqing
Jen, Shyian
Lodes, Michael
Benson, Darin
Jones, Robert
Carter, Darrick
Barth, Brenda
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37.75%
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; ORGANISM: Propioni acnes
PCT-US02-32727-107
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	1434 102 e: 59 166 20	1434)	AsnThrileGluGluArgPro 50 ATACGGCCGCGGCGACCG 387	lyAlaAsnAlaArgLeuVal 70 ::: AAGCAGGATCAGAAT-ATC 446	erLysSerLeuAlaAspVal 89 ::::: crcGAGGAGTTG 497	roThrIleThrLysLeuArgVal 109 :: :: CTCAGCTCCTCGATCTTGCGCTG 536	<pre>spPheGluGluGlyPheGluGlyValAsp 129 TTCGAAAACGGTGGTATTCCC 575</pre>	oGlnProLeuHisGluArgIleAsnGlnAlaLeuSerSerIleGlyAlaLeu 147	laSerValGlnGlnMetile 164 :::::: CCAAGTTACGGTCGCTGTT 695	aArgLysAlaGlyValProValLeulleAsp 177 ::: ::: ACGTCAACTCGGCATTGGTCCTC 747	euLeuThrProAsnLeuSer 197 	uGluGluIleValGluArgGlyMet 217 ::: ::: -GAGGATGATCCTGACGCAGCTTTG 807	hrargSerGluGlnGlyMet 237 	ProLeuHisMetProThrGlnAlaGlnGluValTyr 257 	laAlaThrLeuAlaAlaGly 277 	SerLeuGluGluAlaCysPhePheAlaAsnAlaAlaAlaGlyValValValGlyLys 297 :::
	Length: Matches: Conservativ Mismatches: Indels: Gaps:	-US02-32727-176 (1-	ValProValValLysValAsnThrll ::: :::: CGCCTGCCGTCTTGCGGTGGATACGGGC	aAsnValAlaMetAsnIleAlaSerLeuGlyAl ::: TCGAGGCCTGAGATCGACACTGTGCACGCAAGC	S	SerValProThrHisProThrIleThrLy :: CCTCAGCTCCTCGA	eArgLeuA	oGInProLeuHisGluargIleasnGlnalaLeuSerSerIleGlyAl ::: ::: CAACGAGGCTGGAGTTTTTAGGTGACGCCATCCTTGAAGTTGGTGT	-ValLeuSerAspTyrAlaLysGlyAlaLeuAlaSerValGlnGlnMetll ::::: :::::::::::::::::::::::::::	-GlnLeuAlaArgLysAlaG 	SGlyThrAspPheGluArgTyrArgGlyAlaThrLeuLeuThrProA :::::::: :: -GGATCAAATTGGGCAAGGAGAGGAATTCTCGTCTT	sCysLysThrGlu	uLeuSerAlaLeuLeuValThrArgSer 	AlaProLeuHisMetProT TTCGACGCCGTGGCTGCGG	ThrVallleGlyValLeuA ::: GCTTTCGTTGGTGCGTTGG	PhepheAlaAsnAlaAlaA CGTTTTGCTACCGCGGTGG
OF SEQ ID NOS: 30992 NO 176 H: 1434 DINA ISM: Propioni acnes 32727-176	t Scores: 0.00052: 140.00 Similarity: 35.23% al Similarity: 22.32% .tch: 1	020-325 (1-477) x PCT	Glualapro	GlyGlyAlaAlaAsnValAlaMetAsnIleAlaSerLeuGlyAlaAsnAlaArgLe 	GlyLeuThrGlyIleAspAspAlaAlaArgAlaLeu 	AsnValLysCysAspPheVal :::::: GGAATCCGGTGTGAT	LeuSerArgAsnGlnGlnLeuIl ::: ACGCACCGCTCGTATGCG	ProGlnProLeuHisGluArg ACCAACGAGAGGCTGGAGTTT	ValLeuSerAspTyrAlaLysGlyAlaLeuAlaSerValGlnGlnMetIle		ProLysGlyThrAspPheGlu {:::::::: GGATCAAATTGGGCA	GluPheGluAlaValValGlyLy	LysLeullealaAspTyrGluLeuSerAlaLeuLeuValThrArgSerGluGlnGlyMe ::: ::: :::	SerLeuLeuGlnProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluVal ::: ATCGTCGGCGGGCCGGAAGGGTTCGACGCGTGGCGGCGGCGGCGGACCGTGAAGGCTGTC	AspValThrGlyAlaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAlaAlaGly 	AsnSerLeuGluGluAlaCysPhePheAlaAsnAlaAlaAlaGlyValValValGlyLys :::
; NUMBER OF ; SEQ ID NO ; LENGTH: ; TYPE: DN ; ORGANISM PCT-USO2-327	Alignment S Pred. No.: Score: Percent Sim Best Local Query Match	US-09-912-	Oy 35 Db 328	Oy 51 Db 388	Qy 71 Db 447	Qy 90 Db 498	Qy 110 Db 537	Oy 130 Db 576	Qy 148 Db 636	Qy 165 Db 696	Qy 178 Db 748	Qy 198 Db 784	Oy 218 Db 808	Qy 238 Db 868	Oy 258 Db 925	Qy 278 Db 985

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US-10-092-411A-2746

Sequence 2746, Application US/10092411A

Sequence 2746, Application US/10092411A

Sequence 2746, Application US/10092411A

TGENERAL INFORMATION:
TTILE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 032796-101

CURRENT APPLICATION NUMBER: US/10/092,411A

CURRENT PILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779

SEQ ID NO 2746

SEQ ID NO 2746
                                                                                                                                                                                                                                                       1152 GTGGCCAGGTTGGGGCACACCCAG------1175
                                                                                                                                                                                                                                                                                                                                                                                     1209 CCTCATGAGGTCCCGGTGATTGACCTCGCTGTGGTGCTGGGA------ 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -------TGCTTAATCCCCAATTGTGTGCG-GCG 1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1251 -------ACTCCGAGGTTCCAGGAGTTTCGACGCCATCCTC 1286
                                                                                                                                                                                                                                                                                          371 IleValAlaValAsnSerAspAlaSerThrLysArgLeuLysGlyAspSerArgProVal 390
                                                                   315 -----ArgAlaAspThrGlyPheGlyValMetThrGluGluGluLeuLysLeu 330
                                                                                                                                             331 AlaValAlaAlaAlaArgLySArgGlyGluLySValValMetThrAsnGlyValPheAsp 350
                                                                                                                                                                                                                     351 IleLeuHisAlaGlyHisValSerTyrLeuAlaAsnAlaArgLysLeuGlyAspArgLeu 370
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                                                                                                                                                                                                                                                                                                                                                                  391 Asn-----ProLeuGluGlnArgMetIleValLeuGlyAlaLeuGluAlaValAsp 407
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                            137.50
43.28%
21.64%
5.75%
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Best Local Similarity:
Query Match:
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; CURRENT FILING DATE: 2002-10-11 ; NUMBER OF SEQ ID NOS: 30992 ; SEQ ID NO 132 ; LENGTH: 13380 ; TYPE: DNA ; ORGANISM: Propioni acnes PCT-US02-32727-132	Alignment Scores: 0.0449 Length: 13380 Pred. No.: 133.00 Matches: 124 Score: 34.96% Conservative: 69 Best Local Similarity: 22.46% Mismatches: 183 Query Match: 1 Gaps: 27 DB: 1	US-09-912-020-325 (1-477) x PCT-US02-32727-132 (1-13380) QY	Qy 51 GlyGlyAlaAlaAsnValAlaMetAsnIleAlaSerLeuGlyAlaAsnAlaArgLeu 69 1		Oy 119 LeuAspPheGluGluGlyPheGluGlyValAspProGlnProLeuHisGluArgIleAsn 138	Oy 155 GlyAlaLeuAlaSerValGlnGlnMetIleGlnLeuAlaArgLySAlaGlyValProVal 174	212 IleValGluArgGlyMetLysLeuIleAlaAspTyrGluLeuSerAlaLeuLeu 1130 Ill:::::
Qy 71 GlyLeuThrGlyIleAspAspAlaAlaArgAlaLeuSerLysSerLeuAlaAspValAsn 90	Oy 111 SerArgAsnGlnGlnLeulleArgLeuAspPheGluGluGlyPheGluGlyValAspPro 130 111 bb 295 CTAAAATCAGGTCAAGAAACAGAAATCAATGCACCCGGACCT 336 Oy 131 GlnProLeuHisGluArglleAsnGlnAlaLeuSerSerIle144 112	145 397 163 457 183	Db 517 GTTGAAACAGTATTACCATATCGACCATTATTATTAAACCAAACAAAGATGAATTA 573 Oy 200 GlualaValValGlyLysCysLysThrGluGluIleValGluArgGlyMetLys 218	239 LeuLeuGlnProGlyLysAlaProLeuHisMetProThrGlnAlaGln :::	Db 796 TCCATGGGTCTTAATATAGAAGCTTTTCAACAGGCCGTAGCTTCA 843 Qy 295 ValGlyLysLeuGlyThrSerThr 302 Db 844GGAACAGCGACT 855	PCT-US02-32727-132 PCT-US02-32727-132 Sequence 132, Application PC/TUS0232727 Sequence 132, Applicant Setsing, David Septicant Bhatia, Ajay APPLICANT Maisonneuve, Jean Francois Septicant Wang, Siqing Septicant Wang, Siqing Septicant Septian	PPL

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GRNERAL INFORMATION:
APPLICANT: LYND DOUGETE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES AND THERAPEUTICS
FILE REPRENCE: 03796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT APLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 1139
LENGTH: 432
                    9220 GCCGCCAGCCTATGTCACGGGTTGCTAGAGGGATGGAGCCTCGCCGAGACGATTCAAGCA 9279
                                                                                                                                                                                                                                                          9396 GCATCTGTCATGACGCGCACCCCGCTTATTGACAAGCTGTTAGATCGGCGACTTGCCGAT 9455
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                                                                                                                                                       287 AlaAsnAlaAlaAlaGlyValValValGlyLysLeuGlyThrSerThrValSerProIle 306
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ProThrGlnAlaGlnGluValTyrAspValThr-----GlyAlaGlyAspThrVal 266
                                                                                                                                                                             |||:::|||||||
9280 GCGTCGCCCCACGACGCCGTTGGAGTGTTCCACCGCGATGCCCTCG
                                                                          267 IleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhePhe
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US-09-134-000C-1139
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421 -----IleAlaGlyIleLeuProAspLeuLeuValLysGlyGlyAspTyrLysProGlu 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 TTAGAAAAAAGAAACAAAGT-----TATTTTCATATGAAAACGTAAACAATTATA
                                                                                                                                                                                                                                                                                                  341 LysValValMetThrAsnGlyValPheAspIleLeuHisAlaGlyHisValSerTyrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268 TCCGATATTGCTGAATTTAAAATTGATACTTTAGTCATGGGCGATGATTGGCAAGGGGCT
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GENERAL INFORMATION:

JAPPLICANT: Birse et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA131P1

CURRENT FAPLICATION NUMBER: US/10/264,237

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: PCT/US01/16450

PRIOR APPLICATION NUMBER: US 60/205,515

PRIOR APPLICATION NUMBER: US 60/205,515

NUMBER OF SEQ ID NOS: 2876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            459 GluAspGlyCysSerThrThrAsnIleIleLysLysIle 471
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Mismatches:
                                                                                                                                Matches:
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LOCATION: (919)..(919)
OTHER INFORMATION: n equals a,t,g, or
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; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000c-1139
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LOCATION: (895)..(895)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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50.38%
34.59%
5.47%
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LOCATION: (910)..(910)
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Best Local Similarity:
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LENGTH: 962
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Wed Nov 27 08:37:00 2002

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156 AlaLeuAlaSerValGlnGlnMetIleGlnLeuAlaArgLysAlaGlyValProValLeu 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                470 CTGAGGGCAGCCAATGTCATTAGCAGAGCCAAAGTCATGGTCTGCCAGCTCGAAATA 529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 GAGGTGGCGGCGGTGGTAGTGGTGGCTCCTGCATGACCGAC-----CTGGTCAGTCTT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 ACTICICGITIGCCAAAACIGGA-------GAAACCAICCAIGGA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 CATAAGTITITIATIGGCTITIGGAGGGAAAGGIGCCAACCAGIGIGICCAAGCIGCICGG 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 IleAspPro-----LysGlyThrAspPheGluArgTyrArgGlyAlaThrLeu 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 LeuThrProAsnLeuSerGluPheGluAlaVal------ValGlyLysCysLys 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 ThrGluGluGlu------IleValGluArgGlyMetLysLeuIleAlaAspTyr 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 ThrSerArgIleSerProGluAlaProValProValValLysValAsnThrIleGluGlu 48
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LOCATION: (960)..(960)
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APPLICANT: Carter, Darrick
APPLICANT: Barth, Brenda
APPLICANT: Douglass, John
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32382 CGTGGTGACAAAGCGACTCTC------ATGACACACCGTCACTCGCAATGCC 32426
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                                                                  32325 ATGTCGACGATTCTCAGCTCCGAACGCGGC---TCCCACGTCGAGATTCGTGTCCGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 ValAsnThrIleGluGluArgProGlyGlyAlaAlaAsnValAlaMetAsnIleAlaSer
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                                               243 GlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspValThrGlyAla
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Matches:
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Persing, David
Bhatia, Ajay
Maisonneuve, Jean Francois
Zhang, Yanni
Wang, Siqing
                                                                                                                                      263 GlyAspThrValIleGlyValLeuAla 271
                                                                                                                                                                                             PCT-US02-12727-16; Sequence 16, Application PC/TUS0232727; GENERAL INFORMATION:
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APPLICANT: Skeikv, Yasir
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34.09%
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Benson, Darin
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ORGANISM: Propioni acnes
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Jen, Shyian
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LENGTH: 61557
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Q	32529 CCGCTACGGATAGAGTCCTACGACATTTCCCATATCCAGGGCACCAATGTCGTCGGGTCG		Db 33567 GTGGCCGTCAA
OY Db	121		Qy 376 SerAspAlaSe) :: TCGATGAGACA
QY Db	124 GlyPheGluGlyValAspProGlnProLeuHisGluArgIleAsnGlnAlaLeuSer		Qy 396 ArgMetIleVa: :: Db 33687 GGTGGTCATCT
QY	143 SerIleGlyAlaLeuValLeuSerAspTyrAlaLysGlyAlaLeuAlaSerValGlnGln :::		RESULT 13 US-09-134-000C-1809 ; Sequence 1809, Appl. ; GENERAL INFORMATION
Qy	163 MetIleGlnLeuAlaArgLysAlaGlyValProValLeuIleAspProLysGlyThrAsp	eulleAspProLysGlyThrAsp 182 TTATCGATCCGATTCGATCT	; APPLICANT: Lynn Dou ; TITLE OF INVENTION ; FILLE OF INVENTION ; FILE REFERENCE: 03N
Qy Db	183 PheGluArgTyrArgGlyAlaThrLeuLeuThrProAsnLeu ::::::::::::::::::::::::::::::::::::	ThrProAsnLeu 196 ::: TCGATGGTGGCGCCTCAGGTG 32855	CURRENT APPLICATION CURRENT FILING DATE PRIOR APPLICATION PRIOR PILING DATE:
Oy D	197 SerGluPheGluAlaValValGlyLySCySLySThrGluGluGluIleValGluArgGly ::	luGluGluIleValGluArgGly 216 ::: AGGACGAAATCGCGTTGTGTGGC 32915	; NUMBER OF SEQ ID NO ; SOFTWARE: PatentIn ; SEQ ID NO 1809 ; LENGTH: 810
Q Pb	217 MetLys	LeulleAlaAspTyrGluLeuSerAlaLeuLeuVal 230 :::	; TYPE: DNA ; ORGANISM: Enterocc US-09-134-000C-1809
ογ			Alignment Scores: Pred. No.: Score:
oy d			Best Local Similarity Query Match: DB:
ίδ			US-09-912-020-325 (1-4
qq	33093 GIGTCGGGGCTGGGAGAGACCCGGCGCAAAGGCTCGTCTCCCACTTTGGATCGGTAACG		184
QY	279 SerbeuGluGluAlaCysPhe	PheAlaAsnAlaAla 290 	DB 361 GAGCGCGCGTT
ογ			421
90 :	scririg	AGGCCATCAAC	Db 481 ATTAAATCAC
· 경	ALGYALAYGALGATGTTGACGCCAACGCCC	-ASPInrGIYPhe	Qy 225 LeuSerAlaLeu
Qy	321GlyvalMetThrGluGluGluLys	329	Db 541 ATTGAAGCAGTI
<u>අ</u> දි	330 CCTTGAGCTGTGAGCACCGAGCAGCACGAGGACCCCACGAGTTGTCATTATCACCGGC		601
³ 원	ATTTCTGGTGCTGGGCGTC	GTACCGCAGCTCACGCTGTGGAGGACCTTGGCTGGTACGTC 33446	265
, Qy	Val		DD 658 ACTITITATITGG Qy 284 CysPhePheAla
3 8	357 ValSermvrLenalaasenalaa	GGCCCTCGTTGACGAAATTGCCGCCAATAAC 33506	Db 718 ATTCGTTATGG
연	ATTGATCGCCTAGCGGTGGTTCTCGATGT		
			Db 778 ATTCCTTATCA

Qy Db	372 33567	Valalavalasn
Oy Dp	376 33627	SerAspAlaSerThrLysArgLeuLysGlyAspSerArgProValAsnProLeuGluGln 395 :: :: :: ::
Oy Db 3	396 33687	ArgMetlleValLeuGlyAlaLeu 403 ::: :: GGTGGTCATCTGCTCGACGCCGTT 33710
RESULUTION OF THE PRESULUTION OF	SULT 13 09-134-00C SEQUENCE 18 SEQUENCE 18 APPLICANT: TITLE OF 1 T	RESULT 13 US-09-134-000C-1809 Sequence 1809, Application US/09134000C Sequence 1809, Application US/09134000C Sequence 1809, Application US/09134000C TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES IN 1986-03.2 CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1997-08-15 NUMBER OF SEQ ID NOS: 6812 SOFTWARE: PatentIn version 3.1 SEQ ID NO 1809 TEMENTH: 810 TYPE: DNA
Align Pred. Score Perce Best Query DB:	Alignment Pred. No.: Score: Percent Sil Best Local Query Matc DB:	Alignment Scores: 0.0136 Length: 810 Pred. No.: 120.50 Matches: 38 Score: 120.50 Matches: 28 Best Local Similarity: 44.59% Conservative: 28 Best Local Similarity: 25.68% Mismatches: 61 Query Match: 5.04% Indels: 21 DB: 5
0S-09	-915-	020-325 (1-477) x US-09-134-000C-1809 (1-810)
οy	184	
qΩ	361	GAGCGCGCGGTCGGGGCGACGTCAAATCCCGCACCTGCGTTAGAACAAGTTCCTGAAGAA 420
Qy Db	191	
ΟY	205	LysCysLysThrGluGluGluIleValGluArgGlyMetLysLeuIleAlaAspTyrGlu 224
QQ	481	attaaaatcacagatgaagcgagtatgcgtaaagccgcagaagcacttcatcaattaggg 540
δy	225	LeuSeralaLeuLeuValThrargSerGluGlnGlyMetSerLeuLeuGlnProGlyLys 244 ::: ::::::: aTTGAAGCAGTAATTATACAGTAGTAGTAAAGGCGCCTTTTATGACGTCAATGGACGA 600
Qy d	245	AlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspValThrGlyAlaGlyAsp 264
20		0
Qy	265 658	ThrValileGlyValLeuAlaalaThrLeuAlaAlaGlyAsnSerLeuGluGluAla 283
Qy	284	CysPhePheAlaAsnAlaAlaAlaGlyValValValGlyLysLeuGlyThrSerThrVal 303
Db	718	ATTCGTTATGGAAACAAGCGTCTTCGTTGACTGTTCAACGTTTTGGAGCCCAACCTTCG 777
OY	₹*	SerProlleGluLeuGluAsnAla 311
QQ	178	ATTCCTTATCAACACGAATTGGCA 801

264

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7358 TGCCCAGCGTGCAGATGTGATTATTGGCACGCGTGACGAATTTGATGTCTGGAAAATCA 7299
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                                                                                                                                             -LysCysLysThrGluGluGluIleValGluArgGlyMetLysLeuIleAlaAspTyrGl
                                                                                                                                                                                                                                                                                                                        244 sAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspValThrGlyAlaGlyAs
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TITLE OF INVENTION: Variants of alternative
FILE REPERENCE: 1291B1.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PATENTIN VENTION 3.2
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; Sequence 45787, Application US/09724676
; GENERAL INFORMATION:
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                                                                                                                                                                                              materials incorporating
                                                                                              APPLICANT: Glenn, Matthew
APPLICANT: Havukkala, Ilkka J
APPLICANT: Lubbers, Mark William
APPLICANT: Lubbers, Mark William
APPLICANT: Lubbers, James
TITLE OF INVENTION: Polynucleotides, materials incorpora
TITLE OF INVENTION: them, and methods for using them:
TITLE OF INVENTION: them, and methods for using them:
TILE REPERENCE: 11000.1043 c3
CURRENT APPLICATION NUMBER: US/10/264,213
CURRENT FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 100
LENGTH: 12023
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Mismatches:
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Matches:.
                                                   Sequence 100, Application US/10264213
GENERAL INFORMATION:
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AlaLeuAlaSerValGInGInMetIleGIn :::	uGlullevalGluargGly	yAspThrValileGlyValLe	-ThrGlyPheGlyValMetThrGluGluGluLeuLySLeuAla	pAlaSerThrLysArgLeuly CCAGGAGGTCAATCACTACAL t
AlaLeuValLeuSerAspTyrAlaLysGlyAlaLeuAlaSerValGlnGlnMetIleGln :::	CyslysThrGluGluGluIleVal	AlaGInGluValTyrAspValThrGlyAlaGlyAspThrValIleGlyValLeuAlaAla AlaGInGluValTyrAspValThrGlyAlaGlyAspThrValIleGlyValLeuAlaAla GGGGTGTCCACCACACACCTGGGCC	- B X-4 G	ArgLeulleValAlaValAssSerAspAlaSerThrLysArgLeuLysGlyAsp Arg
AlaLeuvalL GCACGGCCA CEUALARY ATCGCCAAGC 	CysLysThrG	AlaGlnGluv GGGGTGTCCA ThrLeuAlaA ThrLeuAlaA ACCAAAGCC ValValValG	ArgGlyArgAlaAsp- GTGGGCGGAACCCCT ValAlaAlaAlaArgL ::: CAGTTTGCTTCTGGA PheAspIleLeuHisA :::	ArgI SerargProv :: AACTACCCCA TCAGAAGTGG UASPThrF
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Search completed: November 27, 2002, 02:55:41 Job time: 165 secs

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-Qr-Qran2_1/OxPrO_spool/U09912020/runat_20112002_150259_11086/app_query.fasta_1.647
-Qr-Qran2_1/OxPrO_spool/U09912020/runat_20112002_150259_11086/app_query.fasta_1.647
-DB-Genembl .QrMT-fastap -SUFETX=p2nsz_lm300.rge -WINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 .UNITS-bits -START=1 -END--1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=-Ct -THR_MMX=100 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL .OUTFWT=pto -NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-300
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-YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7
                                                                                                    November 24, 2002, 23:18:35 ; Search time 3218 Seconds (without alignments) 4313.871 Million cell updates/sec
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1 MKVTLPEFERAGVMVVGDVM......FEDGCSTINIIKKIQQDKKG
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               GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                          OM protein - nucleic search, using frame_plus_p2n model
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                             327 GluLeuLysLeuAlaValAlaAlaAlaArgLysArgGlyGluLysValValMetThrAsn 346
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                                                                                                                       of microbial genes
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Human polynucleotides and polypeptides encoded thereby
Patent: WO 0190366-A 4327 29-NOV-2001;
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72
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Mahan, M.J., Conner, C.P. and Heithoff, D.M.
Method and probes for the identification of
specifically induced during host infection
Patent: US 6365401-A 186 02-APR-2002;
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Sequence 186 from patent US 6365401.
AR203747
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/db_xref="taxon:9606"
68 c 83 g 41
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73 c 96 g
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/translation="PEAPVQVVDVKDENNRLGGACNVVHNLIALNAQVFVCGVVGNDE AGFWLGEKLESMGVDISYLFVDTSRPTTKKTRVIIANQQVLRVDRES" 41 c 71 q 86 t
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/protein_id="AAL16695.1"
/db_xref="GI:16265978"
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Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
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2 (bases 1 to 273)
6 (bases 1 to 273)
6 (bases 1 to 273)
7 Eng.Y. and Fox.J.G.
Direct Submission
Submitted (09-MAR-2001) Division of Comparative Medicine,
Massachusetts Institute of Technology, 77 Massachusetts Avenue,
Cambridge, MA 02139, USA
1 773
                                                                                                                                                                                                                                             61 GCGTTATGGCGAGCATTAAGGGCGTGGCGATGGTTTTTCGACGAGATACGCCG 120
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Ge,Z., Feng,Y. and Fox,J.G.
Helicobacter hepaticus genome:
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/trans1_table=11
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Helicobacter hepaticus
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/gene="rfaE"
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Peterson, S.N.
Direct Submission
Submitted (13-SEP-1993) Peterson S.N., University of North Carolina Medical School, Microbiology and Immunology, Chapel Hill, NC 27599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 bp DNA linear BCT 29-JAN-1999 random genomic clone hsb8, partial cds.
                                                Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
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Mycoplasma genitalium
Bacteria: Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                    237 MetSerLeuLeuGlnProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluVal 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peterson, S.N., Hu, P.C., Bott, K.F. and Hutchison, C.A. III. A survey of the Mycoplasma genitalium genome by using random sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Characterization and analysis of the Mycoplasma genitalium Thesis (1992) Microbiology and Immunology, University of No Carolina Medical School
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            276 ---AlaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnAlaAlaAlaGlyValVal
                                                                                                Mendrick,D., Porter,M.W., Johnson,K.R., Castle,A.L. and Elashoff,M.R. Molecular toxicology modeling Patent: WO 0210453-A 1264 07-FEB-2002; Gene Logic, Inc. (US)
                                                                                                                                                                                               /organism="Rattus norvegicus"
/db_xref="taxon:10116"
/note="EMBL/GenBank Accession No. A1236089"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.

1 (bassal to 272)
Forsyth, R.A., Ohlsen, K.L. and Zyskind, J.W.
Genes identified as required for proliferation of E. coli
Patent: Wo 0148209-A 89 015-UL-2001;
Elitra Pharmaceuticals, Inc. (US)
                                                                                                                                                         1 CCTGAAGCTCCTGTGCAAGTAGTAGATGTCAAAGATGAAAATAATCGCTTAGGTGGAGCG 60
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                                                                                   ProGlualabrovalProvalvalLysvalAsnThrIleGluGluArgProGlyGlyAla
                                                                                                                                        54 AlaAsnValAlaMetAsnIleAlaSerLeuGlyAlaAsnAlaArgLeuValGlyLeuThr
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Sequence 1264 from Patent W00210453.
AX401588 1 GI:21337768
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                                                          US-09-912-020-325 (1-477) x AF358705 (1-273)
                                                                                                                                                                                                                                                                                                       113 AsnGlnGlnLeuIleArgLeuAspPheGlu 122
                                                                                                                                                                                                                                                                                                                         241 AATCAACAAGTTTTACGCGTAGATAGGGAA 270
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5.01%
       41.118
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Submitted (14-SEP-1999) Organismic & Evolutionary Biology, Harvard
University, 16 Divinity Ave., Cambridge, MA 02138, USA
Location/Qualifiers
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Echinometra mathaei isolate Flc.10 bindin precursor, gene, partial
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Echinometra mathaei
Eukaryota; Metazaa: Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euchinoidea; Echinoea; Echinoida; Echinometridae;
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                                                                                                                                                                                                                                                                                                                                                                                                       242 ProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspValThrGly
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1 (bases 1 to 300)
Palumbi,S.R.
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Palumbi,S.R.
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Submission (14-SEP-1999) Organismic & Evolutionary Biology, Harvard
University, 16 Divinity Ave., Cambridge, MA 02138, USA
Location/Qualifiers
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Echinometra mathaei isolate F1c.7 bindin precursor, gene, partial
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Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinometridae;
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20
39
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Conservative:
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AF186316.1 GI:6318982
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Echinometra mathaei
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Palumbi,S.R.
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Palumbi, S.R.
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69 c 111 g 50 t
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Bacteria, Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
1 (bases 1 to 245)
Forsyth, R.A., Ohlsen, K.L. and Zyskind, J.W.
Genes identified as required for proliferation of E. coli
Patent: WO 0148209-A 90 05-JUL-2001;
Elitra Pharmaceuticals, Inc. (US)
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217 AIGCICGAAGCGAAGCIGAAGGGGAGGGIGAIGAGGACTACAGIAGCAICGCIGAG
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Mismatches:
Indels:
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53 c 55 g 80 t
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Matches:
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Honolulu, HI 96822, USA
Location/Qualifiers
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2.97%
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Best Local Similarity:
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                                                                                                                                     /translation="YGNYPQARNPPMGGGNYPVPGQAPMGQLAQQGYAAPGMGGPVGG
GGGAMAGPFGGGGAGPVGGGGAGPPEFGEMPEAEGAEEEGDKDYSSVDEEETTISAK"
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1 (bases 1 to 300)

Metz, E.C. and Palumbi,S.R.
Positive selection and sequence rearrangements generate extensive polymorphism in the gamete recognition protein bindin

Mol. Biol. Evol. 13 (2), 397-406 (1996)
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinometridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 300)
Metz.C. and Palumbl.S.R.
Direct Submission
Submitted (26-OCT-1995) Edward C. Metz, Zoology, University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 ProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspValThrGly 261
                                                                                                                                                                                                                                                                                                                                                                                                         262 AlaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGlu 281
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110
331
4
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Matches:
Conservative:
Mismatches:
Indels:
              'organism="Echinometra mathaei"
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                                                                                         /product="bindin precursor"
/protein_id="AAF07131.1"
/db_xref="G1:6319068"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 ATGGGTGGACCGGTCGCGGGT------
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                            /isolate="Flc.10"
/db_xref="taxon:31178"
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/product="bindin"
69 c 110 g
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                                                                           /codon_start=1
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U39543.1 GI:1122528
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Best Local Similarity:
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DB:
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/product="bindin precursor"
/protein_id="AAR07091.1"
/d_xref="G1:6319028"
/translation="KGNYPQARNPPMGGGNYPVPGQAPMGGLAQOGYAAPGMGGPVGG
GGGAMAGPIGGGAGPVGGGGGGGAGPPEFEGDNDYSSYDEEETISAK"
                                                                                                                                                                                                                                                                                                                              linear INV 10-NOV-1999 precursor, gene, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (14-SEP-1999) Organismic & Evolutionary Biology, Harvard
University, 16 Divinity Ave., Cambridge, MA 02138, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinometridae;
                                                           242 ProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspValThrGly 261
                                                                                                                                                                                                     -----ATGAGGACTACAGTAGC 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             All males are not created equal: fertility differences depend gamete recognition polymorphisms in sea urchins Proc. Natl. Acad. Sci. U.S.A. 96 (22), 12632-12637 (1999) 20006286
                                                                                                          301 rThrValSerProIleGluLeuGluAsn------AlaValAr
                                                                                                                                                                        313 gGlyArgAlaAspThrGlyPheGlyValMetThrGluGluGluLeuLysLeuAlaValAl
                                          GluAlaCysPhePheAlaAsnAlaAlaAlaGlyValVal-ValGlyLySLeuGlyThrSe
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10
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Mismatches:
Indels:

    .285
    /organism="Echinometra mathaei"
/isolate="Guam3.1"

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Matches:
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Echinometra mathaei
Eukaryota; Metazoa; Echinodermata;
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                                                                                                                                                                                                                                                                ACCEGIGAGGAAGACAACAATTAGTG 295
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/product="bindin"
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AF186277.1 GI:6318943
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69.50
39.22%
29.41%
2.90%
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1 (bases 1 to 285)
Palumbi, S.R.
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Palumbi, S.R.
              112 ATGGGTGGACCGGTCGGTGGT
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Query Match:
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VERSION
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GGGAMAGPIGGGAGPVGGGGAGPPEFGGMSEEEGAEGEGDEDYSSTGEEETTISAK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 300)
Palumbi, S.R.
Direct Submission
Submitted (14-SEP-1999) Organismic & Evolutionary Biology, Harvard University, 16 Divinity Ave., Cambridge, MA 02138, USA
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Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinometridae;
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                                                                          Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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/protein_id="AAF07095.1"
/db_xref="GI:6319032"
                                             Length:
Matches:
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                                                                                                                          Gaps:
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                                                                                                                                                       (1-245)
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a 69 c 113
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AF186281.1 GI:6318947
                                          7.93e+03
70.00
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100.00%
2.93%
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70.00
38.18%
28.18%
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Echinometra mathaei
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Palumbi,S.R.
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Best Local Similarity:
Query Match:
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VERSION
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TITLE
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AUTHORS
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LOCUS
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242 ProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluvalTyrAspValThrGly 261
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69.50
39.22%
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Echinometra mathaei
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Palumbi, S.R.
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Palumbi, S.R.
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AF186282.1
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GGGAMAGPIGGGAGPVGGGGAGPPEFGEMPEEEGDKDYSSVDEEETTISAK"
                                                                                                                                                                                                                                                                                                                               AF186279 285 bp DNA linear INV 10-NOV-1999
Echinometra mathaei isolate Guam4.1 bindin precursor, gene, partial
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Submitted (14-SEP-1999) Organismic & Evolutionary Biology, Harvard
University, 16 Divinity Ave., Cambridge, MA 02138, USA
Location/Qualifiers
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Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinometridae;
                                                                                              218 -TGCCCGAAGAGGAGGGTGATAAGGACTACAGTAGCGTCGATGAGGAAGAGACAACAATT 276
                                                                                                                                  301 rThrValSerProIleGluLeuGluAsnAlaValArgGlyArgAlaAspThrGlyPheGl 321
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CCCGGTCAAGCACCT----ATGGGTCAGCTAGCCCAACAAGGTTACGCTGCTCCTGGA 111
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                           262 AlaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGlu 281
                                                                              282 GluAlaCysPhePheAlaAsnAlaAlaGlyValVal-ValGlyLysLeuGlyThrSe
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Conservative:
Mismatches:
Indels:

    285 /organism="Echinometra mathaei"

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/product="bindin precursor"
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                                                    112 ATGGGTGGACCGGTCGTGGT-----
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AF186279.1 GI:6318945
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Echinometra mathaei
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Palumbi, S.R.
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Palumbi,S.R.
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GGGAMAGPIGGGAGPVGGGGAGPPEFGEMPEEEGDKDYSSVDEEETTISAK"
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Submitted (14-SEP-1999) Organismic & Evolutionary Biology, Harvard
University, 16 Divinity Ave., Cambridge, MA 02138, USA
Location/Qualifiers
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Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinometridae;
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262 AlaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGlu 281
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                                                                                                                                                        282 GluAlaCysPhePheAlaAsnAlaAlaAlaGlyValVal-ValGlyLysLeuGlyThrSe
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/isolate="Guam5.2"
/db_xref="taxon:31178"
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GGGAIAGPIGRGAGPVGGGGAGPPEFGEMPEEEGDKDYSSVDEEETTISAK"
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Echinometra mathael isolate Guam7.1 bindin precursor, gene, partial
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Submitted (14-SEP-1999) Organismic & Evolutionary Biology, Harvard
University, 16 Divinity Ave., Cambridge, MA 02138, USA
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Echinometra mathaei
Eukaryota; Metazoa: Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea: Euechinoidea; Echinosea; Echinoida; Echinometridae;
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                                                                                   282 GluAlaCysPhePheAlaAsnAlaAlaAlaGlyValVal-ValGlyLysLeuGlyThrSe 301
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                                                                 242 ProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspValThrGly 261
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    /organism="Echinometra mathaei"

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Palumbi, S.R.
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Palumbi, S.R.
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                                                                                                                                                                                                                                                            262 AlaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGlu 281
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                                  Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: November 25, 2002, 00:20:07 Job time : 3221\ \mathrm{secs}
                                                                                                                          US-09-912-020-325 (1-477) x AF186284 (1-285)
                                                                                                                                                                                                                                                                                                 112 ATGGGTGGACCGGTCGTGGT------
                                                                                   Gaps:
           39.22%
29.41%
2.90%
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341 sVal 342
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SUMMARIES

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(without alignments)
3653.752 Million cell updates/sec
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/ SIDS2/ggdata/geneseqn emb1/NA1989.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                               OM protein - nucleic search, using frame_plus_p2n model
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2393
1 MKVTLPEFERAGVMVVGDVM.
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Maximum DB seq length: 300
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Perfect score:
Sequence:
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Pred. No. is the number of results.predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Resi	sult No.	Score	Query Match	Length	DB	ID	Description
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•	٦ ٥	162	- œ	243	18	ABN / / 21 / AAT 6744 5	Human OKFZ164 CDNA
t	۹ ۳	120		272	22	AAH81290	scherichia coli
ט	4	112		292	24	ABK63357	t sequence di
	2	7.		285	24	ABL75687	þ
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1	۲,	٠ <u>.</u> ر	m (300	20	AAZ14636	uman gene expres
บ	00	٠,		242	77	AAH61291 ABI:74436	Corn tassel-derive
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	11			279	21	ABQ63223	Mycobacterium bovi
	12	9		237	22	AAH52260	Human AFP protein
	13	64		275	24	ABL38371	Human colon tumour
υ	14	co.		298	24	ABL76194	Corn tassel-derive
υ	15	63.5		267	22	AAK17810	Human brain expres
O	9 :		٠	267	22	AAK43661	bone marr
υ	17			267	22	AA149/02	Probe #18388 used
O	20 0		٠	797	7.7	AA109966	Probe #995/ used t
	5 6	٠.	•	784	2 6	AASBOOLS	UNA encoding novel
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ပ	17	70		L 4 2	77	AAA14323	Oligonaciectide 3
ţ	77	7 0	٠	140	22	AAA14524 AAS02280	Sunthetic oligodeo
ı	24	2 6		671	2 0	AAS02288	Synthetic Oligodeo
υ	25	62		245	22	ABA88721	Escherichia coli p
)	26	62		252	21	AAA14575	Sequence map of a
υ	27	62		258	21	AAA14570	Sequence map of a
	28	62		283	22	ABA12944	Human nervous syst
ပ	59	61.5		225	15	AAQ57460	NADH-ubiquinone ox
	30	ä		299	19	AAV20211	Ε,
	31	61	•	176	24	ABL63015	Breast cancer rela
	3.5	5		264	10	AAT 25654	Human gene Signatu
ပ	5 C	۔ م		224	24	AAT03309 ABK80353	e rra
		5 o		248	77	ABK81018	
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U	37			286	20	AAV87597	EST clone DY959.
	38	9.		294	23	AAS54270	Pseudomonas aerugi
O	39	29		117	22	ABA71890	foetal live
υ	40	29	•	117	22	AAK20273	brain exp
υ	41	29	•	117	22	AAK46346	e marr
O	42	29		117	22	AAI52242	#20928 use
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	4.	200		197	19	AAV31991	S106 polynuci
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ΚM	ъ	- rn	itor		cytokine;	11 proliferati	on; cell differentiation;
Υ		ne mod	lat); haematopoiesi	topo	iesis regulation;	sue growth;
X Z	ang1	anglogenes1		activin; inhib	inhib	in; chemotactic;	chemokinetic; naemostatic;
X	hehe	hehavionr.	בשטמפט	₹.	fora	tive disorder.	al disorder.
ΚW	carc	liovasc	ular dis	ĕ	i mai	ystem disor	
KW	tiss	tissue growth d		, rd	tissue	r.e	rder; diabetes mellitus;

vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; neuroprotective; antitatherosclerotic; anticoadulant; thrombolytic; cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide; gene; ss. hypothyroidism; cholesterol ester storage disease; infection; vulnerary;

Homo sapiens.

WO200190366-A2.

29-NOV-2001.

24-MAY-2001; 2001WO-US17076

24-MAY-2000; 2000US-206690P

(CURA-) CURAGEN CORP.

Shimkets RA; Leach MD,

WPI; 2002-106200/14 P-PSDB; ABP33191 Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ transplantation

Claim 1; Page 1338; 2508pp; English.

designated ORF (open reading frame) 1-4534, and sequences ABN75054ABN79587 represent cDNAs encoding them. The invention also encompasses
Delypeptides at least 80% identical to the ORF1-ORF4534 (collectively
referred to as ORFX) proteins, polynucleotides at least 85% identical to
Delypeptides at least 80% identical to the ORF1-ORF4534 (collectively
referred to as ORFX) proteins, polynucleotides at least 85% identical to
Delypeptides, the recombinant production of ORFX proteins, antibodies
competition of the ORFX proteins, antibodies
pecific for ORFX proteins, methods of detecting ORFX polynucleotides and
polypeptides, methods of screening individuals for a predisposition to an
ORFX-associated disorder. The ORFX proteins of the invention have a wide
range of biological activities, such as cytokine, cell proliferation,
cell differentiation, immune modulation, haematopoiesis regulation,
tissue growth, anglogenesis, activin or inhibin activity, chemotactic/
chemokinetic activity, haemostatic activity, tumour inhibition activity,
and antihinfective activity, and may also be involved in the determination
of bodily characteristics, fertility and behaviour. ORFX proteins,
cof bodily characteristics, fertility and behaviour. ORFX proteins,
cof cher proliferative disorders such as psoriasis and benign tumours,
cof conter proliferative disorders such as psoriasis and benign tumours, cardiovascular diseases, immune system disorders claimed to corgan transplantation, disorders of tissue growth and regeneration, disorders of tissue growth and regeneration, diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester storage disease, and infectious diseases caused by viral, bacterial, fungal and other pathogens. ORFX nucleic acids may also be used as a source of primers and probes, in the detection of ORFX genomic sequences or transcripts, in the identification and clouing of homologous sequences, in genetic diagnosis, be used to produce transgenic animals mucleic acids may additionally be used to produce transgenic animals which may be useful for studying the function and/or activity of ORFX protein, and in drug screening. The ORFX proteins may also be used as immunogens to generate specific antibodies, which are useful in the neurological disorders such as epilepsy and Alzheimer's disease,

51 A; 68 C; 83 G; 41 T; 0 other; BP; Sequence 243

diagnosis, treatment and monitoring of ORFX-associated diseases

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243
32
20
27
0
        Length:
Matches:
Conservative:
Mismatches:
                                               Indels:
         59e-07
               170.00
65.82%
40.51%
7.10%
                                    Best Local Similarity:
                           Percent Similarity:
Alignment Scores:
                                            Query Match:
          Pred. No.:
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This sequence encodes a H. pylori cytoplasmic protein.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino
                                                                                                                         417
                                                                                                                                                                                                         378 AlaSerThrLysArgLeuLysGlyAspSerArgProValAsnProLeuGluGlnArgMet 397
                                                                                                                                                        61 GCCGTTATGGCGAGCATTAAGGGCGTGGCGATGGTCACGTTTTTTCGACGAGATACGCCG 120
                                                                                                                                                                                       418 GlnArgLeuIleAlaGlyIleLeuProAspLeuLeuValLysGlyGlyAspTyrLysPro 437
                                                                           Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bolypeptide(s) - useful for vaccines to treat or prevent H. pylori
Infection, and to detect Helicobacter
                                                                                                                                                                                                                                                     GluGluIleAlaGlySerLysGluValTrpAlaAsnGlyGlyGluValLeuValLeu 456
                                                                                                                                                                                                                                                                       398 IleValLeuGlyAlaLeuGluAlaValAspTrpValValSerPheGluGluAspThrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori nucleic acid sequences and related
                                                                                                                                                                                                                                                                                                                                                                                                                                         H. pylori cytoplasmic protein ORF 21742157.aa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/note= "no stop codon given"
Gaps:
                               US-09-912-020-325 (1-477) x ABN77217 (1-243)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Page 176; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                               AAT67445 standard; DNA; 249 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96WO-US09122
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95US-0487032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-052306/05.
P-PSDB; AAW20221.
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The present invention describes a purified or isolated nucleic acid asquence (I) consisting essentially of one of the 93 nucleotide sequences given in AAH81202 to AAH81294, where expression of the nucleic acid in a microorganism is capable of inhibiting proliferation of a microorganism.
homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                                           GluAspThrProGlnArgLeuIleAlaGlyIleLeuProAspLeuLeuValLysGlyGly 433
                                                                                                                                                                                                                                                                                                                                                                                                                ||||||||| |:::||||:: |||||||::
GACTACCTCAATAAAGGAAGTCATAGGGAGCGAG------TTGGCTAAAGAAACC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 CGTTTGATAGAATTTGAAGAGGTTATTCCACAAGGCGCTATCATAGAAAAAATTAAAAAGG 237
                                                                                                                                                                                                                                                                                                                                                                                               AspTyrLysProGluGluIleAlaGlySerLysGluValTrpAlaAsnGlyGluVal 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                      454 LeuValLeuAsnPheGluAspGlyCysSerThrThrAsnIleIleLysLysIleGlnGln 473
                                                                                                                                                                                                                                                                                                       10 AAAGACAGGGCGTTTCTTTTAGCGAGCTTGTCTTGCGTGGATTAJGTTGTGGTGTTTGGA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids encoding proteins required for Escherichia coli
proliferation, useful for screening for antimicrobial agents -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli; identification; proliferation; microorganism; antimicrobial; antibacterial; antibiotic; gene therapy; diagnosis; bacterial growth inhibition; ds.
                                                                                                                                            249
35
17
24
4
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                                                                                                84 A; 39 C; 62 G; 64 T; 0 other;
                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 128; 596pp; English.
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162.00
65.00%
43.75%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ELIT-) ELITRA PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-457376/49.
                                                                                                                                                                                      Best Local Similarity:
                                                                                                Sequence 249 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli
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                                                                                                                                                                        Percent Similarity
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                                                                                                                             Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH81290;
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(I) have antibacterial and antiblotic activities, and can be used in gene therapy. Expression of (I) in a microorganism inhibits proliferation of the microcranism, and the manufactured antiblotic is useful for reducing the activity or level of a gene product required for proliferation of a microorganism in a subject, specifically humans. The nucleic acids that inhibit bacterial growth or proliferation can be used as antisense therapeutics for Killing bacteria. In addition to therapeutic applications, the nucleic acid sequences complementary to exequences required for proliferation can be used as diagnostic tools. For example, nucleic acid probes complementary to proliferation-required sequences that are specific for particular species of microorganisms can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat sequence differentially expressed in response to a hepatotoxin #1264.
                                                                                                                                                                                                                 represent oligonucleotides, which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                         be used as probes to identify particular microorganism species in
clinical specimens. AAH81295 to AAH81487 encode the Escherichia coli
proteins given in AAG98239 to AAG98431, and AAH81488 to AAH81491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening; differential expression; centrilobular necrosis; steatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Elashoff MR;
                                                                                                                                                                                                                                                                                                        272
23
23
0
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                                                                                                                                                                                                                                                                                                                      Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357/c
ABK63357 standard; cDNA; 292 BP.
                                                                                                                                                                                                                                                           Sequence 272 BP; 65 A; 61 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001US-290645P.
2001US-292336P.
2001US-295798P.
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2001US-298884P.
2001US-303459P.
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2001US-290029P
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100.00%
100.00%
5.01%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENE-) GENE LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-241625/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     475 LysLysGly 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 AAAAAAGGC 203
                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                  present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200210453-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-NOV-2000;
11-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUN-2001;
                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mendrick D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK63357;
                                                                                                                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                         Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK63357,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
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Predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells

Claim 1; Seq ID No 1264; 239pp; English.

The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the compounds or the progression in tissues or cells exposed to the toxic contain and comparing these to gene expression in unexposed tissues or cells. Also included are methods of predicting at least one toxic effect of a compound or progression of a toxic effect, preferably the hepatotoxicity of a compound, comprising detecting the level of expression in a tissue or cell sample exposed to the compound of two or cepsness is indicative of at least one toxic effect or progression of the genes is indicative of at least one toxic effect or progression. Compare genes is indicative of at least one toxic effect or progression. The method can also be used to identify an agent which modulates the coxic response and predict cellular pathways that a compound modulates in a conformation and actions under the specification, a computer of a comprising a set of at least two probes (on a solid support in kit form), where each of the probes comprises a sequence that specifically hybridises to a gene listed in the specification, a computer of system comprising at least two genes listed in the specification, and a user interface to view the information used to present information identifying the expression level in a tissue or cell of at least one gene classification. The method is useful for elucidating global changes in gene expression and for identifying toxicity markers in the proposed to a known toxin. The genes and the companion and toxicity markers in the proposed to a known toxining the genes and a present information and toxicity markers in the prediction and and proviet the same and and toxicity markers in the proposed to a known toxining the specification. state of tissue or cell tag (EST) or cDNA derived from a gene in response to a hepatotoxic agent. toxicity markers in drug screening and toxicity assays. The genes and gene expression information may be used as diagnostic markers for the prediction or identification of the physiological state of tissue or sample that has been exposed to a compound or agent. Hepatoctoxicity characterised by centrilobular necrosis and steatosis. The present sequence is an expressed sequence which is differentially expressed

Sequence 292 BP; 67 A; 60 C; 86 G; 79 T; 0 other;

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237 MetSerLeuLeuGlnProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluVal 256
                                                                                                                                                                       278 GTGACACTGTCACAGGCAGAACCTGTTCCAAAGCACATTCCCACAGAAGCAGTCAAGGGT 219
                                                                                                                                                                                                                 257 TyraspValThrGlyAlaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAla--- 275
                                                                                                                                                                                                                                 218 GTGGACACCACGGTGCTGGTGACATTTGTGGGAGCGCTTGCCTTCTACCTGGCTTAC 159
                                                                                                                                                                                                                                                                              276 ---AlaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnAlaAlaAlaGlyValVal 294
                                                                                                                                                                                                                                                                                                           158 TACCCAAGTCTGTCCTTGGAAGAAATGCTCAAGAGATCTAATTCCATCGCTGCGGTCAGC 99
                 292
29
10
30
20
1
                Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                            ValGlyLysLeuGlyThrSerThrValSerPro 305
                                                                                                                                                                                                                                                                                                                                                                         98 GICCAGGCCACAGGAACACAGTCCTCTTATCCA 66
                                                                                              Gaps:
                                                                                                                       US-09-912-020-325 (1-477) x ABK63357 (1-292)
                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL75687 standard; cDNA; 285 BP
              0.102
112.00
54.93%
40.85%
4.68%
                                             Percent Similarity:
Best Local Similarity:
Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL75687;
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DB:
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-- LeuLysLeuAlaVal 332

328

316 AlaAspThrGlyPheGlyValMetThrGluGluGlu----

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US-09-912-020-325 (1-477) x ABL75687

285 26 13 27 23

Conservative: Mismatches: Indels:

107.50 43.82% 29.21% 4.49%

Percent Similarity: Best Local Similarity:

Score:

Query Match:

0.257

Alignment Scores:

Gaps:

Matches: Length:

Sequence 285 BP; 65 A; 60 C; 74 G; 82 T; 4 other;

(or more) nucleic acid sequences.

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The present sequence describes a purified corn tassel-derived polynucleotide sequence (cdps) comprising a nucleic acid sequence selected from those given in ABL70637 to ABL70833. The cdps sequences encode corn tassel-derived polypeptides (CDPs). The cdps sequences (I) can be used for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid breeding programs. (I) are also useful in the evaluation, and alteration of desired characteristics associated with growth and development, disease resistance, environmental adaptability, quality and yield, and as molecular markers for studying inheritance of multigene traits in a plant breeding program. (I) can be used to produce a tassel-specific profile of gene transcription, a transcript image, to clone regulatory elements for use in transformation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel purified corn tassel-derived polynucleotide useful for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vectors, to express a polypeptide, to identify, isolate or extend identical or related corn tassel nucleic acid sequences from DNA libraries, in nucleic acid hybridisation or amplification technologies, as query sequences to determine homology of known sequences, as probe for use in Southern or Northern hybridisation, and to identify the presence of and/or to determine the degree of similarity between two
                                                                           Corn; corn tassel-derived polynucleotide; cdps; hybrid breeding; CDPs; inheritance; characteristic; growth; development; disease resistance; environmental adaptability; quality; yield; molecular marker; multigene trait; plant breeding; corn tassel; gene; ss.
                                       Corn tassel-derived polynucleotide (cdps) SEQ ID NO:5061.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID 5061; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sherman BK;
                                                                                                                                                                                                                                                                                                          99US-0294093
                                                                                                                                                                                                                                                                                                                                                98US-082567P
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lalgudi RV, Ito LY,
                                                                                                                                                                                                                                                                                                                                                                                                                             SHERMAN B K.
                                                                                                                                                                                                                                                                                                                                                                                     LALGUDI R V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-163647/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                breeding programs
                                                                                                                                                                                                                          US2001051335-A1.
                                                                                                                                                                                                                                                                                                                                                21-APR-1998;
14-MAY-2002
                                                                                                                                                                                                                                                                                                          16-APR-1999;
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                                                                                                                                                                                    Zea mays.
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(SHER/)
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The present invention describes a library of human polynucleotides comprising the sequences given in AAZ12532 to AAZ17779. Also described is method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell
                                                                                                                                                                                           58 ATCGTGAGCTTCGGCGAGATGCTCATTGAC------TTCGTCCCGACCGTGTCGGGG 108
                                                                                                                                                                                                                                                                                                                    ----GGGTTCCTCAAGGCCCCC 147
                                                                                                                                                                                                                                                                                                                                                                                                                  ValMetValValGlyAspValMetLeuAspArgTyrTrpTyrGlyProThr---SerArg 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; gene; gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 ValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLeuSerLysSerLeuAlaAspVal
                                                                                                                                                                                                                                                        32 IleSer---ProGluAlaProValProValValLysValAsnThrIleGluGluArgPro
                                                                                                                                                                                                                                                                                                                                                                                    51 GlyGlyAla---AlaAsnValAlaMetAsnIleAlaSerLeuGlyAlaAsnAlaArgLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human gene expression product cDNA sequence SEQ ID NO:2105.
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Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA:
Jones WL, Kassam A, Kennedy GC, Kita D, Labat 1;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human genes and their expression products which are differentially expressed in different cell types
                                                               US-09-912-020-325 (1-477) x AAA67292 (1-300)
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                                                                                                                                                                                                                                                                                             268 GGGGTCAACTGCGACGGCATCAAC 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 AsnValLySCysAspPheValSer 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
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98US-0072910.
98US-0075954.
98US-0080114.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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(HYSE-) HYSEQ INC
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31-MAR-1998;
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                                                                                                                                                                                                                             Bucalyptus grandis; pinus radiata; Monterey pine; modification;
plant cell wall; polysaccharide; polysaccharide biosynthetic pathway;
transgenic plant; ds.
61 GTGAAAAGTCAGCTATCTCATANCCTTCCAACTTCTCGCCGGATCATGCAGTTTTCAAAT 120
                                                               333 AlaAlaAlaArgLysArgGlyGluLysValValMetThrAsnGlyValPheAspIleLeu 352
                                                                                                                        121 GGGCAGGCTCCTTCGCCAGGTGCTCGTGTTGTAGTAGATGGCACATTTGATCTTTTC 180
                                                                                                                                                                                        353 HisAlaGlyHisValSerTyrLeuAlaAsnAlaArgLysLeuGlyAspArgLeuIleVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New genes encoding proteins involved in a plant polysaccharide blosynthetic pathway, useful for modulating or altering the polysaccharide content, composition or structure of the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eucalyptus grandis D-fructokinase DNA sequence SEQ ID NO:293.
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Matches:
Conservative:
Mismatches:
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(FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                                                                                                                    373 AlaValAsnSerAspAlaSerThrLys 381
                                                                                                                                                                                                                                                                                                                                                                                 241 GTATCTATGGACGACGNATCGANTCAG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 150; 301pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA67292 standard; DNA; 300 BP.
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99US-0148426
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84.50
51.14%
31.82%
3.53%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eucalyptus grandis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bloksberg LN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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11-AUG-1999;
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20-APR-2000

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(ELIT-) ELITRA PHARM INC.

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of the 5248 polynuclectide sequences given in AAZI2532 to AAZI7779. The polynuclectides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynuclectides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynuclectides may also be used to construct arrays for diagnostics (which may be used to determine function of an arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polynucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, and lung cancer. The polynucleotides can also be used to screen for
    where the gene product is encoded by one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 LeuGlnProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspVal 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 ACAGAGCAAAGTCCCTGGGCCCTGGGAAAAGCCTCATCACGGCCAGGGCTCTGGCCCATA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 GluAlaValValGlyLysCysLysThrGluGluGluIleValGluArgGlyMetLysLeu 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220 IleAlaAspTyrGluLeuSerAlaLeuLeuValThrArgSerGluGlnGlyMetSerLeu 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 GTCGGAGGCCAGCAACTACCTGCACTT-----GCCGCCAAGAGTGGGCAATCTTTT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 AGGTCTCTCGGGAAGGCCCCAGCCTCCCTCCCACTGAAGAAAAGAAGTTGGTA---ACC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 ThrGlyAlaGlyAspThrVallleGlyValLeuAlaAla-------ThrLeu 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 GAGCAGACCCCAGGGCCTCTTAGCCAATCCCCGGCCTGGTGAAGCAGGCGAAGCAGATG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli, identification, proliferation, microorganism, antimicrobial; antibacterial; antibiotic, gene therapy; diagnosis; bacterial growth inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        275 AlaAlaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnAla 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               249 GTGGCTGGACAGACACTGGCACAGTCTTGCTGCTGCTGGGAGC 293
                                                                                                                                                                                                                                                                                                                                                                                                                  300
21
23
42
9
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                                                                                                                                                                                                                                                                                                                                                      Sequence 300 BP; 70 A; 89 C; 92 G; 49 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-912-020-325 (1-477) x AAZ14636 (1-300)
                                                                                                                                                                                                                                                                                            and lung cancer. The polynucleotide peptide analogues and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH81291 standard; DNA; 245 BP.
suspected of being cancerous,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                    576
71.50
46.32%
22.11%
2.99%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
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Score:
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.9-DEC-2000; 2000WO-US34419. 23-DEC-1999; 99US-0173005

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The present invention describes a purified or isolated nucleic acid
sequence (I) consisting essentially of one of the 93 nucleotide sequences
given in AAHB1294, where expression of the nucleic acid in a
microorganism is capable of inhibiting proliferation of a microorganism.

(I) have antibacterial and antibiotic activities, and can be used in
gene therapy. Expression of (I) in a microorganism inhibits proliferation
of the microorganism, and the manufactured antibiotic is useful for
reducing the activity or level of a gene product required for
reducing the activity or level of a gene product required for
cucleic acids that inhibit bacterial growth or proliferation can be used
as antisense therapeutics for killing bacteria. In addition to
therapeutic applications, the nucleic acid sequences complementary to
sequences required for proliferation can be used as antisense that are specific for particular species of microorganisms can
be used as probes to identify particular species of microorganisms can
clinical specimens. AAHB1295 to AAHB1487 encode the Escherichia coli
proteins given in AAG98229 to AAG8431, and AAHB1488 to AAHB1491

represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corn; corn tassel-derived polynucleotide; cdps; hybrid breeding; CDPs; inheritance; characteristic; growth; development; disease resistance; environmental adaptability; quality; yield; molecular marker; multigene trait; plant breeding; corn tassel; gene; ss.
                                                                                               Novel nucleic acids encoding proteins required for Escherichia coli
proliferation, useful for screening for antimicrobial agents -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corn tassel-derived polynucleotide (cdps) SEQ ID NO:3810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 G; 80 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
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Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-912-020-325 (1-477) x AAH81291 (1-245)
                              Zyskind JW;
                                                                                                                                               Claim 1; Page 129; 596pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL74436 standard; cDNA; 287
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100.00%
100.00%
2.93%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAY-2002 (first entry)
                                Ohlsen KL,
                                                               WPI; 2001-457376/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 245 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL74436;
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Mycobacterium tuberculosis; Mycobacterium bovis; mycobacterium;
             Eucalyptus grandis.
                                       WO200022092-A2
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                                                                                                                                                                                                        polynucleotide sequence (cdps) comprising a nucleic acid sequence selected from those given in ABL70627 to ABL76833. The cdps sequences encode corn tassel-derived polypeptides (CDP9). The cdps sequences (I) can be used for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid breeding programs. (I) are also useful in the evaluation, and alteration of desired characteristics associated with growth and development, disease resistance, environmental adaptability, quality and yield, and as molecular markers for studying inheritance of multigene traits in a plant breeding program. (I) can be used to produce a tassel-specific profile of gene transcription, a transformation vectors, to express a polypeptide, to identify, isolate or extend identical or related corn tassel nucleic acid sequences from DNA is for use in nucleic acid hybridisation or amplification technologies, as query sequences to determine homology of known sequences, as probe for use in Southern or Northern hybridisation, and to identify the presence of and/or to determine the degree of similarity between two
                                                                                                                   determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317 AspThrGlyPheGlyValMetThrGlu-------GluGluLeuLySLeuAla 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 ValAlaAlaAlaArgLysArgGly------GluLysValValMetThrAsnGly 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eucalyptus grandis; pinus radiata; Monterey pine; modification; plant cell wall; polysaccharide; polysaccharide biosynthetic pathway; transgenic plant; ds.
                                                                                                                                                                                                The present sequence describes a purified corn tassel-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eucalyptus grandis D-fructokinase DNA sequence SEQ ID NO:279.
                                                                                                     corn tassel-derived polynucleotide useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 287
18
6
20
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
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                                                                                                                                                                      Claim 1; SEQ ID 3810; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  or more) nucleic acid sequences.
                                                  Sherman BK;
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67.50
45.28%
33.96%
2.82%
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                                                    Ito LY,
                       SHERMAN B K.
LALGUDI R V.
                                                                             WPI; 2002-163647/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                             breeding programs
                                                                                                       Novel purified
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                                                    RV,
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           (ITOL/)
(SHER/)
                                                    Lalgudi
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Q
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The present invention describes isolated polynucleotides (PN) comprising a sequence selected from one of 835 nucleotide sequences given in AAA67073 to AAA67907, their (reverse) complements, sequences given in AAA67073 to AAA67907, their (reverse) complements, sequences producing an Expectation (B) value of 0.01 or less compared to the 835 sequences at least 50% identical to them, 200, 100, 40 or 20-mers of the 835 sequences that are degenerately equivalent or allelic to the 835 sequences. The polynucleotides are used to modify the activity of a polypeptide involved in a polysaccharide biosynthetic polysaccharide content, romposition or structure of the plant. AAB16268 to AAB16340 are proteins encoded by some of the polynucleotide sequence given in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 ThrGlyAlaGlyAspThrVallleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSer 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 ATTCTCGAAGATGAAGGAAAATTGAGGAAAGTCCTGAAGTTTGCAAACGCGTGCGGAGCC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 ValValValGlyLysLeuGlyThrSerThrValSerProIleGluLeuGlu 309
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17
5
27
7
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Mismatches:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
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                                                                                                                                                                                                                    (FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                        (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 146; 301pp; English.
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                                                   99WO-NZ00169
                                                                                                        98US-0170862
                                                                                                                               99US-0148426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.50
40.35%
29.82%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.788
                                                                                                                                                                                                                                                                                                                       WPI; 2000-339328/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                    3loksberg LN;
                                                                                                        13-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                   08-OCT-1999;
                                                                                                                                     11-AUG-1999;
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20-APR-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                      The present invention describes a method for isolating a polynucleotide of interest that is present or is expressed in a genome of a first mycobacterium strain and that is absent or altered in a genome of a second mycobacterium strain, which is different from the first strain using a bacterial artificial chromosome (BAC) vector. Recombinant BAC vectors, which are preferably immobilised, can be used to detect mycobacterial nucleic acids (genomic DNA, cDNA or mRNA) in biological samples. The polynucleotides identified are useful as probes or primers for detecting a given mycobacterium of interest. BAC vectors it is possible to physically map a polynucleotide of mycobacterial origin in a polynucleotide and vectors from the present invention are useful in providing information for combating tuberculosis. It is possible to compare genomes between different strains or species and section of the present information are useful in providing information for combating tuberculosis. It is possible to compare genomes between different strains or species and ABBA1227 to ABBA1220 represent sequences used in the cemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              310 AsnAlaValArgGlyArgAlaAspThrGlyPheGlyValMetThrGluGluGluLeuLys 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           279
detection; BAC vector; bacterial artificial chromosome; tuberculosis;
                                                                                                                                                                                                                                            useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 GCTGGCGTGGCCAGGACGAGATCCCGACGATTGGGGC-AGATGCCTGCTCACCATCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               330 LeualaValAlaalaAlaArgLysArg-----GlyGluLysValValMetThrAsnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValPheAspIleLeuHisAlaGlyHisValSerTyrLeuAlaAsnAlaArgLysLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolation of polynucleotides from mycobacterial genomes, detection of Mycobacteria and for combating tuberculosis
                                                                                                                                                                                         Billault A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             279
22
6
72
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 279 BP; 37 A; 94 C; 105 G; 43 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                            Gordon S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-912-020-325 (1-477) x ABQ63223 (1-279)
                                                                                                                                                                                                                                                                                  Claim 27; Page 127; 161pp; English.
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                                                                                                                                                                                            Buchrieser-Brosch R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.88e+03
65.50
46.67%
36.67%
2.74%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH52260 standard; cDNA; 237
                                                                                                                 99WO-IB00740.
                                                                                                                                        98US-0060756
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                                                                                                                                                                   INSP ) INST PASTEUR
                                                                                                                                                                                                                   WPI; 2000-013262/01.
                                     bovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                     Mycobacterium
                                                             WO9954487-A2
                                                                                                                16-APR-1999;
                                                                                                                                         16-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-SEP-2001
                                                                                      8-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH52260;
             dene; ds.
                                                                                                                                                                                            Cole S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  348
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g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
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AAH52093 to AAH52303 encode the human secreted proteins given in AAG81242 to AAG81453. The secreted proteins can be used for directing the secretion of proteins of interest from a host cell including bacteria, fungal cells, and cultured higher entaryotic cells. The present invention also describes fusion proteins, where a secreted protein of the invention protein selected from the group consisting of maltose binding protein, an immunoglobulin constant region, a polyhistidine tag and a peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 ProGlnProLeuHisGluArgIleAsnGlnAlaLeuSerSerIleGlyAlaLeuValLeu 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 SerAspTyrAlaLysGlyAlaLeuAlaSerValGlnGlnMetIleGlnLeuAlaArgLys 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 AlaGly------ValProValLeuIleAspProLysGlyThrAspPheGluArgTyr 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 GTTGGGAAAGTTGTGTTCCCGAGACTACAGGATAAAAATACTATGAT---AAGAAATAC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated polypeptide for directing secretion of proteins of interest from a host cell including, e.g. bacteria, includes contiguous amino acid residues of polypeptide with specified amino acids \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 GGTGCCTGTGCCTCAGGGGATTTCGCTTCTGTACAGGAAGCAATGGCAAAAATGAGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 CCTGTGGTCCTGTCGCAAGAGGTGGAGTCCGTTCTT-----GTGGGTGCTGCTGTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 ArgGlyAlaThrLeuLeuThrProAsnLeuSerGluPheGluAlaValVal 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 CAAGTATTCCTGAAGCTGGTTGAACACCAGAAGGAGTATTTGGCGATCATG 225
                                              Human; secreted protein; secretion; bacterial cell; fungal eukaryotic cell; fusion protein; maltose binding protein; immunoglobulin constant region; polyhistidine tag; ss.
Human AFP protein encoding cDNA sequence SEQ ID NO:335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237
24
12
35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Page 556; 617pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                   990S-0160712
                                                                                                                                                                                                                                                                                                                                                        20-OCT-2000; 2000WO-US29052
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46.75%
31.17%
2.67%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ZYMO) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-300340/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yee
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                                                                                                                                                                                                                                   WO200129221-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                   20-0CT-1999;
                                                                                                                                                                               Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conklin DC,
                                                                                                                                                                                                                                                                                              26-APR-2001
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ABL38371
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BP.

ABL76194 standard; cDNA; 298

(first entry)

14-MAY-2002

ABL76194;

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US-09-912-020-325 (1-477) x ABL76194 (1-298)
                         ABL76194/c
RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated colon tumor polynucleotide differentially expressed in colon tumor or colon metastatic tumor and polypeptides encoded by them, useful for inhibiting development of cancer in patient -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291 AlaGlyvalValValGlyLysLeuGlyThrSerThrValSerProIleGluLeuGluAsn 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 AlaValArgGlyArgAlaAspThrGlyPheGlyValMetThrGluGluGluLeuLysLeu 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331 AlavalAlaAlaAlaArgLysArgGlyGluLysValValMetThrAsnGlyValPheAsp 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------IleLeuHisAlaGlyHisValSerTyrLeuAlaAsnAlaArgLysLeuGly 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 ATGGAATCCATGGTCCATGCAGACACAAGATCATTATTCTGAAGAAGCCAAAGCTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer; colon tumour antigen; cytostatic; vaccine; metastatic antigen; diagnosis; gene; ss.
                                                                         Human colon tumour antigen polynucleotide SEQ ID NO:1960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGGAAGTAGTGGCACCAAACCAAGAGTCGGGGATGAAG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AspArgLeuIleValAlaValAsnSerAspAlaSerThrLys 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G; 54 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-912-020-325 (1-477) x ABL38371 (1-275)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID 1960; 105pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.53e+03
64.00
39.36%
24.47%
2.67%
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20-FEB-2001; 2001US-270216P.
                                                                                                                                                                                                                                                                                                                                                                              08-JUN-2001; 2001WO-US18557
                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jiang Y, Harlocker SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-114514/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity:
                                                                                                                                                                                                                                                                     WO200196388-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                               ; colon
                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 275
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DB:
                                                                                                                                                               colon
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9
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Diprucleotide sequence (cgss) comprising a nucleic acid sequence selected from those given in ABL70627 to ABL76833. The cdps sequences can be used from those given in ABL70627 to ABL76833. The cdps sequences can be used for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid breeding programs. (I) are also useful in the evaluation, and alteration of desired characteristics associated with growth and development, disease resistance, environmental adaptability, quality and yield, and as molecular markers for studying inheritance of multigene traits in a plant breeding program. (I) can be used to produce a tassel-specific profile of gene transcription, a transcript image, to clone regulatory elements for use in transformation vectors, to express a polypeptide, to identify, isolate or extend the corn tassel nucleic acid sequences from DNA contraction technologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           libraries, in nucleic acid hybridisation or amplification technologies, as quences to determine homology of known sequences, as probe for use in Southern or Northern hybridisation, and to identify the presence of and/or to determine the degree of similarity between two
                                                                                                                           cdps; hybrid breeding; CDPs;
                                                                                                                                          inheritance; characteristic; growth; development; disease resistance; environmental adaptability; quality; yield; molecular marker; multigene trait; plant breeding; corn tassel; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence describes a purified corn tassel-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               purified corn tassel-derived polynucleotide useful for
                                                                                       Corn tassel-derived polynucleotide (cdps) SEQ ID NO:5568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298
25
14
14
18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches:
Conservative:
Mismatches:
                                                                                                                           tassel-derived polynucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID 5568; 201pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (or more) nucleic acid sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sherman BK;
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                                                                                                                                                                                                                                                                                                                                                               98US-082567P.
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                                                                                                                                                                                                                                                                                                                                                                                                   (LALG/) LALGUDI R V.
                                                                                                                                                                                                                                                                                                                                                                                                                                     (SHER/) SHERMAN B K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-163647/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  breeding programs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                     US2001051335-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 298
                                                                                                                                                                                                                                                                                                                            16-APR-1999;
                                                                                                                                                                                                                                                                                                                                                               21-APR-1998;
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55 G; 64 T; 0 other;

66 A; 82 C;

Sequence 267 BP;

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probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single exon nucleic acid probes for analyzing gene expression in human brains -
                                                                             177 GGGCTCAGAAGCCAGGGGTTGGTGGCGCCAATGATCTTGCGGCCAGTTGTGACGACGCT 118
                             297 CCAATCAGCAGGGCCCTCGGGGAACCNCAGGGCAATCTCCTTATTAGCACTCTCAATGCT 238
                                                                                                                                                                                       LeuAlaAspValAsnValLysCysAspPheValSerValProThrHisProThrIleThr 105
                                                                                                                                                                                                                                                   106 LysLeuArgValLeuSerArgAsnGlnGlnLeuIleArgLeuAspPheGluGluGlyPhe 125
                                                                                                                        82
                                                                                                                                                                                                                     94
                                                                                                                                                                                                                                                                                   ----CACAGGGCCAGAGATGATGTAGTCCACGAGGCCCTGGAAGAAGGCCTT 46
ProThrSerArgIle-----SerProGluAlaProValProValValLysValAsnThr 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
epilepsy; cancer; ss.
                                                                                                                        66 AsnAlaArgLeuValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLeuSerLysSer
                                                           46 IleGluGluArgProGlyGlyAlaAlaAsnValAlaMetAsnIleAlaSerLeuGlyAla
                                                                                                                                                                                                                    Example 4; SEQ ID NO: 17801; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human brain expressed single exon probe SEQ ID NO: 17801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                              AAK17810/c
ID AAK17810 standard; DNA; 267 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen W,
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
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27-SEP-2000; 2000US-0236359
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                                                                                                                                                                                                                               152 TIGGGAGTGAGCTCTIGIGAGTCACAGGTIGGGGCTTCCCTGTGAACCTGGTGAGGCTC
                                                                                                                                                                                                                                                      73 ThrGlyIleAsp-----AspAlaAlaArgAlaLeuSerLysSerLeuAlaAspVal
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23
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17
                                Conservative:
Mismatches:
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Matches:
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-MODEL-frame+_p2n.model -DEV-xlp
-Q-C9012_L/1098/app_query.fasta_1.647
-Q-C9012_L/102POL_209012020/runat_20112002_150300_11098/app_query.fasta_1.647
-Q-C9012_L/102POL_209001/020912020/runat_2011200_150300_11098/app_query.fasta_1.647
-UNITS-bits -START-fastap -SUFFIX*P2DRS_In300_rst -MINATCH=0.1 -LOOPEXT=0
-UNITS-bits -START-1 -END=-1 -MATRIX*biosum62 -TRANS=human40.cdi -LIST=45
-DOOFALIGN=200 -THR_SCOREP=CT -THR_MXX=100 - AIRR_MINGN=15 -MODE=LOCAL
-OUTFMT-btc -NORM=axt -HBAPSIZE=500 -MINEN-0 -MAXLEN-30
-USER-US09912020_eCGN_1_1_2024_erunat_20112002_150300_11098 -NCPU=6 -ICPU=3
-NO.XLPXY -NO.MANP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGIGG -DEV_TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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3265.109 Million cell updates/sec
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                                                  Compugen Ltd
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compuc
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Listing first 45 summaries
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Maximum DB seq length: 300
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Processory Courty	Sult Score Match Length DB ID 2	cript.
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Japanese medaka. Oryzias latipes Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthomorpha; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

VERSION KEYWORDS SOURCE ORGANISM ACCESSION

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Marray.M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="OLEO6.08a"
/clone_lib="Medaka liver cDNA library (OLe) from HNI"
/tissue_type="liver"
/dev_stage="adult" 37 t
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This clone was isolated from Medaka liver cDNA library (OLe).
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Naruse,K., Mitani,H. and Tanaka,M.
Medaka EST Project in University of Tokyo (2001)
Unpublished (2001)
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/organism="Oryzias latipes"
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Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Best Local Similarity:
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                            REFERENCE
AUTHORS
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AIZJ6U89 292 bp mRNA linear EST 31-JAN-1999 EST232651 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone ROVDES93' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: embryo; Vector: pBluescribe (modified);
Site_1: MluL; Site_2: SalI; Cloned unidirectionally from
mNA prepared from 13,500 2-cell stage embryos. Primer:
SalI(dT): 5'-CGTCGACGCTCATTTTTTTTTTTTTTTTTTTTTTT-3',
were cloned into the MluI/SalI sites of a modified
pBluescribe vector using commercial linkers (NEB).
Average insert size: 1.2 kb."
5 4 c 53 g 15
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Washington University School of MedicineP
4444 Forest Park ParkWay, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@Watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351 IleLeuHisAlaGlyHisValSerTyrLeuAlaAsnAlaArgLysLeuGlyAspArgLeu 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
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Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333 AlaalaAlaargLysArgGly-----GluLysValValMetThrAsnGlyValPheAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GCTGCGGCACAAATTAGCGGAGTAGCCATGAAAACGGTCATCACCTTCGGCACCTTCGAT
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The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
                                                                                                                                                                                                                                                                                                           /clone_lib-"Knowles Solter mouse 2 cell"
/close_type="embryo"
/dev.stage="2-cell"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371 IlevalAlaValAsnSerAspAlaSerThrLysArgLeuLysGly 385
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27
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                       /strain="C57BL/6J x DBA/2J F1"
/db_xref="taxon:10090"
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Matches:
                                                                                                                                                                                                                                                /organism="Mus musculus"
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Query Match:
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us-09-912-020-325.p2nszlm300.rst

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H32797 238 bp mRNA linear EST 02-APR-1998 EST108244 Rat PC-12 cells, untreated Rattus sp. cDNA clone RPCCJ755 end similar to Cholinephosphate cytidylyltransferase, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l (bases 1 to 238)
Lee, N.H., Weinstock, K.G., Kirkness, E.F., Earle-Hughes, J.A., Fuldner, R.A., Marmaras, S., Glodek, A., Gocayne, J.D., Adams, M.D., Kerlavage, A.R., Fraser, C.M. and Venter, J.C.
Comparative expressed sequence-tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="RPCGJ75"
/clone_lib="Rat PC-12 cells, untreated"
/clone_lib="Rat PC-12 cells, untreated"
/note="Vector: pBluescript SK-; Site_l: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_l: EcoRI; Site_2:
XhoI; poly(A)+ RNA was purified from untreated PCl2 cells cultured for 9 days. cDNA was constructed using an oligo-dT primer and directionally cloned using the Lambda SAP II Vector Kit by Stratagene"
63 c 68 g 52 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                  343 ValMetThrasnGlyValPheAspIleLeuHisAlaGlyHisValSerTyrLeuAlaAsn 362
                                                                                                                                                                                                                                                                                                                                                                                               144 AATAAAGGTCCA-----CCAGTTATGAATGAACAAGAAAGA-----TATAAAGCA 188
                                                                                                                                                                                                                                       24 GITIAIGITGATGGITGTTITGATTTAATGCATTITGGACATGCAAATGCATTAAGACAA 83
                                                                                                                                                                                                                                                                                        363 AlaargLysLeuGlyAspArgLeuIleValAlaValAsnSerAspAlaSerThrLysArg
                                                                                                                                                                                                                                                                                                                            383 LeuLysGlyAspSerArgProValAsnProLeuGluGlnArgMetIleValLeuGlyAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 92, 8303-8307 (1995) 95396786
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GTACGTGCATGTAAATGGGCAGATGAAGTTGCAGAAGGTGCACCT
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                                                                                        Conservative:
Mismatches:
Indels:
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/db_xref="ATCC (inhost):2002922"
/db_xref="taxon:10118"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Lee, NH
The Institute for Genomic Research
712, Medical Center Drive, Rockville, MD
7712, Medical Center Drive, Rockville, MD
7713, Mall: 301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
For clone availability please contact th
(tdbinfo@tdb.tigr.org)
Seq primer: M13 Reverse.
                                                      Length:
Matches:
                                                                                                                                               Gaps:
                                                                                                                                                                                (1-240)
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                                       Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:44689"
/clone="SSE551"
/clone_lib="Dictyostellum discoldeum SS (H.Urushihara)"
                                                                                    MetSerLeuLeuGlnProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluVal 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIGACACTGTCACAGGCAGAACCTGTTCCAAAGCACATTCCCACAGAAGCAGTCAAGGCT 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 TyrAspValThrGlyAlaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAla--- 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 GTGGACACCACGGTGCTGGTGACAGTTTTGTGGGAGCGCTTGCCTTCTACCTGGCTTAC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276 ---AlaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnAlaAlaAlaGlyValVal 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 TACCCAAGTCTGTCCTTGGAAGAAATGCTCAAGAGATCTAATTCCATCGTGGGGTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        project in Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Developmental cDNA in Dictyostellum discoideum (1999) Unpublished (1999) Contact: Hideko Urushihara Institute of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota: Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 240)
Urushihara,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Tsukuba
11-11 Tennouda1, Tsukuba, Ibaraki 305-8572,
Tel: 81-298-53-6614
Fax: 81-298-53-6614
                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: hidekoebiol.tsukuba.ac.jp
PROJECT - Dictyostelium discoideum cDNA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValGlyLysLeuGlyThrSerThrValSerPro 305
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                                                      Location/Qualifiers
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EST.
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                  Email: nhiee@tigr.org
Seg primer: M13-21.
Fax: (301)-838-0208
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112.00
54.93%
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163 AATAAAGGTCCA-----CCAGTTATGAATGAACAAGAAAGA------TATAAAGCA 207
                                      363 AlaArgLysLeuGlyAspArgLeuIleValAlaValAsnSerAspAlaSerThrLysArg
                                                                 383 LeuLysGlyAspSerArgProValAsnProLeuGluGlnArgMetIleValLeuGlyAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Dictyostelium discoideum"
/strain="AA4"
/db_xref="taxon:44689"
/clone="SSK263"
/clone="Ib="Dictyostelium discoideum SS (H.Urushihara)"
/dev_stage="slug"
/dev_stage="slug"
/dev_stage="slug"
                                                                                                                                                                                                                                      359 TyrLeuAlaAsnAlaArgLysLeuGlyAspArg-----LeuIleValAlaValAsnSer 376
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Unpublished (1999)
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Dictyostelium discoideum
Eukaryota: Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 240)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Hideko Urushihara
Institute of Biological Sciences
Institute of Taukuba
University of Taukuba
U-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@blol.tsukuba.ac.jp
PROJECT - Dictyostellum discoideum cDNA project in project in coation/Qualifiers
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AU074294.1 GI:5180715
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343 ValMetThrAsnGlyValPheAspIleLeuHisAlaGlyHisValSerTyrLeuAlaAsn 362

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1. (bases 1 to 300)

Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo, K., Suyama,A. and Sugano,S.

In silico mapping of the 5'-ends of human mRARs using full-length enriched and 5'-end enriched cDNA libraries constructed by Oligo-capping method enriched cDNA libraries constructed by Unpublished (2001)

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
5. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
                                                                                                                    AU100188
AU100188 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone REC00707 similar to Homo sapiens mRNA for phosphoethanolamine CYtidylyltransferase, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/do_xef="taxon:5606"
/clone="RECO0707"
/clone=lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"
3 90 c 117 g 40 t
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403 LeuGluAlaValAspTrp 408
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BF755713 242 bp mRNA linear EST 12-JAN-2001
PM4-CT0562-291000-002-910 CT0562 Homo sapiens cDNA, mRNA sequence.
BF755713
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1 (bases 1 to 242)
1 
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
  324 ThrGluGluGluLeuLysLeuAlaValAlaAlaAlaArgLysArgGlyGluLysValVal 343
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/clone="MXLV (Nsf Xylem Late wood vertical)"
/tissue_type="primary xylem"
/dav_stage="late wood"
/lab_host="Xil-Blue"
/lab_host="Xil-Blue"
/note="Vector: pTriplEx; Site_1: EcoRI; The library is
from late (summer-August) wood, taken from below the crown
of a 20 year old tree. The harvested xylem tissue was on
the the cusp between transitional and mature wood. NOTE:
The sequences contain a 'CDNA adapter' between the EcoRI
site and the start of the EST. The adapter sequence is
/ANTCGGCCATTANGGCC."
71 t i8 others
                                                                                                                                                                                                                                                                                                           235 bp mRNA linear EST 12-MAR-2002 Clone NXLV_079_E07_F NXLV (Nsf Xylem Late wood Vertical) Pinus taeda cDNA BM903102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 235)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain-"Coastal plain loblolly pine from North Carolina" /db_xref-"taxon:3352"
                                          133 GATGGCTGCTATGACATGGTGCATTACGGCCACTCCAACCAGCTGCGCCAGGCACGGGCC 192
                                                                                           366 LeuGlyAspArgLeuIleValAlaValAsnSerAspAlaSerThrLysArgLeuLysGly 385
                                                                                                                    236 GlyMetSerLeuLeuGlnProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGlu 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecular Basis of Wood Formation in the Pine Megagenome Unpublished (2000)
Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu
                                                                                                                                                                                    386 AspSerArgProValAsnProLeuGluGlnArgMetIleValLeuGlyAlaLeu 403
                                                                                                                                                                                                                                   CCC-----CCGGTGTTCACTCAGGAGGAGATACAAGATGGTGCAGGCCATC 300
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Unpublished (2000)
Contact: Yoshihide Hayashizaki
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URL:http://genome_gsc.riken.go.jp,
URL:http://genome_gsc.riken.go.jp,
Carninci.P. Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the Synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninoi,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                         EST 29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute Sciences Center(GSC), Tokohama Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 202)
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musculus CDNA clone A130033M23 3', mRNA sequence.
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Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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344 MetThrasnGlyValPheAspIleLeuHisAlaGlyHisValSerTyrLeuAlaAsnAla 363
                               364 ArgLysLeuGlyAspArg-----LeuIleValAlaValAsnSerAspAlaSerThrLys 381
                                                                                                                                                             103 CACAGGCTGGCAGAGGCCCTACATCATCGCGGCTTACACTTTGACCAGGAGGTCAAT 44
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/clone_lib="RIKEN full-length enriched, 16
                                                                                                                                                                                                                   382 ArgLeuLysGlyAspSerArgProValAsnProLeuGlu 394
                                                                                                                                                                                                                                                                             43 CACAACAAGGGGAAGAACTACCCCATCATGAATCTGCAA 5
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/dev_stage="16 days neonate"
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AW565187 19-JUL-2000 LG1_328_B07.b1_A002 Light Grown 1 (LG1) Sorghum bicolor cDNA, mRNA
/note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Ist strand cDNA was primed with a primer [8].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sorghum bicolor
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC
clade, Panicoideae, Andropogoneae, Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 ValThrGlyAlaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsn 278
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hens, GA 30602-7271, USA
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Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C. and Pr.
An EST database from Sorghum: light-grown seedlings
Unpublished (2000)

Contact: Cordonnier-Pratt MM
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Fax: 706 583 0210
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Mismatches:
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BQ634379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: cou@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW782015
297 bp mRNA linear EST 03-DEC-2001
s199e02.91 Gm-c1027 Glycine max CDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1027-7539 5' similar to TR:Q92V19 Q92V19 PUTATIVE
PHOSPHOETHANOLAMINE CYTLDYLYLTRANSFERASE. ;, mRNA sequence.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                         1. 150
/dprantsm="Sorghum bicolor"
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/clone_lib="Light Grown 1 (LG1)"
/note="Yorgan: 10- to 14-day-old light-grown (greenhouse)
/note="Yorgan: 10- to 14-day-old light-grown (greenhouse)
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/note="Yorgan: 12- to 14-day-old light-grown"
/note="Yorgan: 12- to 14-day-old light-grown"
/note="Yorgan: 12- to 14-day-old light-grown"
/note="Yorgan: 13-day-old light-grown"
/note="Yorgan: 13-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349 PheAspIleLeuHisAlaGlyHisValSerTyrLeuAlaAsnAlaArgLysLeuGlyAsp 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369 ArgLeuIleValAlaValAsnSerAspAlaSerThrLysArgLeuLysGlyAspSerArg 388
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 TTTGATCTCATGCACTACGGCCATGCAATGCATTGCGGCAGGTAAGTTGCTGGGAGAT
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Public Soybean EST Project
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Seq primer: JEN REV
High quality sequence stop: 25
POLYA-No.
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                                                                                                            Location/Qualifiers
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Fax: 314 286 1810
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/ADD. TAILOSE—TO THOUGH TO THOUGH WATER COYLEGORS of 3 and 7-day old Williams seedlings which were propagated on paper towels with distilled water. The cotyledons were flash-frozen in liquid nitrogen, then lyophilized for 72 hours. Unequal amounts of mRNA was used for cDNA synthesis. Stratagene's cDNA synthexix Kit (catalog number 200401) was used to synthexiz the cDNA. First- stranded synthesis was performed with 5-methyl dCTP, hone the ligated CDNA was performed with 5-methyl dCTP, hone the ligated cDNA was performed synthesis primer was used. An anchor nucleotide (V-A. C. or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGAAACATAGTTCTCAG(T)18] to anchor the primer at the 5' end of the poly(A) tract. After second strand synthesis, the CDNA ends were filled in with cloned Pfu DNA, ligated to ECORI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis, the CDNA master strand synthesis primer was then restricted by their hemimethylated status. The CDNA constructs were size-fractionated with a 500 bp cutoff, using Gibcobal Life Technologies' CDNA Size Fractionation Stratagene's BBluescript (IM) II XR Fracdigested vettor (PBluescript II SK(+) that has been digested with ECORI and XhoI, and phosphorylated by Stratagene). 97% of the white and Dhue colonies appear to contain recombinant plasmids with CDNA has the ECORI and XhoI, and phosphorylated by Stratagene). 97% of the white and Dhue colonies appear to contain recombinant plasmids with CDNA has the Pack Dased on size (n=30). This bilbrary was constructed by Dr. Paul Keim and Dr. Virginia COYPAIL.
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NXRV068_C02_F NXRV (Nsf Xylem Root wood Vertical) Pinus taeda cDNA clone NXRV068_C02 5', mRNA sequence.
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                                                                                                                                                                                                                                /tissue_type="cotyledons of 3- and 7-day-old Williams seedlings"
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                                                                                                                                     /db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1027-7539"
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High quality sequence stop: 195.
Location/Qualifiers
                                                                                                 /organism="Glycine max"
                                                                                                                                                                                                          /clone_lib="Gm-c1027
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                                                                                                                                                                                                                                                                                                                                                                        irom juvenile wood to mature wood production. NOTE: The sequences contain a 'CDNA adapter' between the EcoRI site and the start of the EST. The adaptersequence is 'AATTCGGCACGAG'."
                                                                                                                                                                                          1. .249
/organism="Pinus taeda"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 249)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------GTCCCCACGGTCTCGGATGTTTCGTTGGCTGAAGCGCCCGGATTC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 CAAAAGGCTGCAAGTGGTGCACCTGCTAATGTGGCTGTTGGAATTTCCAGGCTCGGTGGC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 AsnAlaArgLeuValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLeuSerLysSer 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 ValMetValValGlyAspValMetLeuAspArgTyrTrpTyrGlyProThrSerArgIle 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 SerProGluAlaProValProValValLysValAsnThrIleGluGluArgProGly---
                                                                                                                                                                                                                                                    /clone="NXRV068_C02"
/clone_lib="NXRV (Nsf Xylem Root wood Vertical)"
/tissue_type="Xylem"
                                                         Molecular Basis of Wood Formation in the Pine Megagenome
                                                                                                                                                                                                                                                                                                                                                                                                                                              5 others
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                                                                                                                                                                                                                                                                                             /cell_type="Root (primary)"
/dev_stage="Transitional"
/lab_host="XL1-Blue"
                                                                     Unpublished (2000)
Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-912-020-325 (1-477) x BQ634379 (1-249)
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                                                                                                                                                                             Location/Qualifiers
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                                            Sederoff, R.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Pinus, Pinus.
1 (bases 1 to 268)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 ValProValValLysValAsnThrIleGluGluArgProClyGlyAla---AlaAsnVal
                                                                    Molecular Basis of Wood Formation in the Pine Megagenome Unpublished (2000)
Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu
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                                                     Sederoff, R.
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AL Upublished (1996)
Contact: Brummet SR: Robb F
Brummet, Sequencing RaD
Amersham Life Science, Inc.
Amersham Life Science, 26101 Miles Rd, Cleveland, OH 44128
Tel: 2164649277; 4102348896
Email: cn28601075: 4102348896
Email: cn28601075: 4102348896
Email: cn28601076: Location/Qualiflers
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Search completed: November 25, 2002, 00:59:48 Job time: 2371 secs

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Sequence 65, Appl
Sequence 3, Appl1
Sequence 3, Appl1
Sequence 2, Appl
Sequence 190, App
Sequence 2418, App
Sequence 1, Appl1
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APPLICANT: Conner Mr., Christopher P.
APPLICANT: Conner Mr., Christopher P.
APPLICANT: Hiethoff Mr., Douglas M.
TITLE OF INVENTION: METHOD AND PROBES FOR THE IDENTIFICATION
TITLE OF INVENTION: OF MICROBIAL GENES SPECIFICALLY INDUCED DURING HOST
TITLE OF INVENTION: INFECTION
NUMBER OF SEQUENCES: 255
CORRESPONDENCE: ADDRESS:
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US-08-818-111-39

US-09-056-556-39

US-09-075-848-9

US-09-175-848-9

US-08-154-418-5

US-08-154-418-5

US-08-154-418-5

US-08-105-168B-7

US-08-105-168B-7

US-08-105-168B-7

US-08-105-168B-7

US-08-105-168B-5

US-08-105-168B-5

US-08-105-168B-3

US-08-105-168B-3

US-08-105-168B-3

US-08-105-168B-3

US-08-105-168B-3

US-08-105-168B-1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 186, Application US/08651155B Patent No. 6365401
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
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NAME: Petersen Mr., Steven C.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 17060.1
TELEPHONE: 303/546-1300
TELEFAX: 303/449-5426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: ABA1475
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         -MODEL=frame+_pro.model_DEV=xlp
-0=/cgn2_1/USPTO_spool/US09912020/runat_20112002_150300_11121/app_query.fasta_1.647
-0=/cgn2_1/USPTO_spool/US09912020/runat_20112002_150300_11121/app_query.fasta_1.647
-DB-fssued_Patents_NA -QFWT=fastap -SUFFIX=pb1ssin300.rni -MINAATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=300 -USER=US09912020_eCOL_1__38_erunat_20112002_150300_11121 -NCPU=6
-ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_IIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                                                                                    November 24, 2002, 23:20:29; Search time 74 Seconds (without alignments) 1976.822 Million cell updates/sec
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                               GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-060-756-722
US-08-716-942-22
US-09-130-337A-22
US-08-105-168B-4
US-08-698-948-4
US-09-060-756-209
US-08-818-111-37
US-09-072-556-37
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Maximum Match 100%
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Fgapop 6.0, Fgapext
Delop 6.0, Delext
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1110987634351

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COUNTRY:
 Query Match:
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APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Bordon, Stephen
APPLICANT: BILlault, Alain
TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLECTIDE OF INTEREST FROM
TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
FILE REFERENCE: 3495-0169
CURRENT APPLICATION NUMBER: US/09/060,756
CURRENT FILING DATE: 1998-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . LOCATION: (various positions within the sequence)
: OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-060-756-722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                287 AlaAsnAlaAlaAlaGlyValValValGlyLysLeuGlyThrSerThrValSerProIle 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluLeuGluAsnAlaValArgGlyArgAlaAspThrGlyPheGlyValMetThrGluGlu 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       327 GluLeuLysLeuAlaValAlaAlaAlaArgLysArgGlyGluLysValValMetThrAsn 346
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                                                                                                                                                                                                                                                                                                                                                                         267 IleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhePhe
                                                                                                                                                                                                                                                                                                                                                                                            2 ATCGGCGTGCTGGCGGCGACCTG-GCCGCGGAAATACCCTGGAAGAGGCGTGTTATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 GlyValPheAspIle---LeuHis-----AlaGlyHisValSerTyrLeu 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 ---GCGTTCGATATCTGACGCCATTATGACGCAACTGGACCTATCGGATACTTA 281
                                                                                                                                                                                                           294
72
6
12
10
5
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                             Length: Matches:
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; Patent No. 6183957
                               LENGTH: 294 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
 186:
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                                                                                                                                                                                                          1.33e-20
263.00
79.59%
73.47%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 743
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 722
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65.50
36.15%
27.69%
INFORMATION FOR SEQ ID NO:
                  SEQUENCE CHARACTERISTICS
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APPLICANT: Cole, Stewart
                                                                                                                                                                                                                                                                    Best Local Similarity:
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APPLICANT: Terragen Diversity Inc.
APPLICANT: Radomski, Christopher C. A.
APPLICANT: Seow, Kah Tong
APPLICANT: Warren, R. Antony J.
APPLICANT: Yap, Wai Ho
TITLE OF INVENTION: METHOD FOR ISOLATING XYLANASE GENE
TITLE OF INVENTION: SEQUENCES FROM SOIL DNA, COMPOSITIONS USEFUL IN SUCH METHOD
TITLE OF INVENTION: COMPOSITIONS OBTAINED THEREBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 ATTGGGGC-AGATGCGTGCTCACCATCGGGGTATTTGACGGGGTGCACGCGGGGACGCC 250
                                                                                                                               240 LeuGlnProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspVal 259
                                                                                                                                                                                                                                                                       LeuGluGluAlaCysPhePheAlaAsnAlaAlaAlaGlyValValValGlyLysLeuGly 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320 PheGlyValMetThrGluGluGluLeuLysLeuAlaValAlaAlaAlaArgLysArg--- 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 GTAGGCTTG------CGATCGTGCAGCGCTGGCGTGGCCAGGACGAGATCCCGACGACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --- GlyGluLysValValMetThrAsnGlyValPheAspIleLeuHisAlaGlyHisVal 357
                                                                                                                                                                111 111 ::::::111 3 CTGGGACCACGGTGCTCCCGGACGTGCTGCGCCCAGGTG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 ThrSerThrValSerProlleGluLeuGluAsnAlaValArgGlyArgAlaAspThrGly
                                                                                                                                                                                                                                      260 ThrGlyAlaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSer
40
                                                                          US-09-912-020-325 (1-477) x US-09-060-756-722 (1-280)
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
Onevaring SYSTEM: DOS 5.0
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Indels:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/004,157
FILING DATE: 20-Sep-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22, Application US/08716942
Patent No. 5849491
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REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Word Perfect
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2.748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MABILAT et al.
TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE
TITLE OF INVENTION: MYCOBACTERIA
                                                                                                                                                                                                                                                                                                                                                                                                           204 GTGGCTCCCAGGCGCCCACGCGCGCCGTCGTCACCTGCTCGTTGACGAC 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 CGTGATGTAGGCGGCGTAGGCGTCGCGAAACGCGCCGGCGGCGTCGCTGACCAGGCGCTCGAA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 ArgLeuValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLeuSerLysSerLeuAla
; OTHER INFORMATION: Description of unknown organism: soil microbe US-09-130-337A-22
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ZIR: Virginia
ZIR: Virginia
ZIR: Z3314
                                                                                                                                             Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                       US-09-912-020-325 (1-477) x US-09-130-337A-22 (1-294)
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Matches:
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CURRENT APPLICATION DATA:
FILING DATE: AUGUST 12, 1993
APPLICATION NUMBER: US/08/105,168B
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: FR9210094
FILING DATE: AUGUST 8, 1992
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                 Gaps:
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MEDIUM TYPE: 3.5" DS/HD
COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: William P. Berridge
REGISTRATION: NUMBER: 30,03
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TELEFAX: (703) 836-2787
INFORMATION FOR SEQ ID NO: 4:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: 3liff & B
STREET: 700 South Wa
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                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                   Alignment Scores:
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No.:
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APPLICANT: Warren, RAJ
APPLICANT: Warren, RAJ
APPLICANT: Warren, RAJ
TITLE OF INVENTION: METHOD FOR AMPLIFICATION OF XYLANASE GENE FRAGMENTS
TITLE OF INVENTION: FROM SOIL DNA, COMPOSITIONS USEFUL IN SUCH METHOD AND COMPOSITIC
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 9993-004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 GGGGTCGCCGCGTGGGCCAGTTCATAGGCGAAGCGCATGTTCCAGCGGTCCGAGCGC 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 GlyValMetValValGlyAspValMetLeuAspArgTyrTrpTyrGlyProThrSerArg
                                                                                                                                                                                                                                                                                                                  fragment of xylanase gene from degenerate primer amplification of soil DNA
                                                                                                                                                                                                                                                                                                                                                                                                                          294
27
16
37
4
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Matches:
Conservative:
Mismatches:
Indels:
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CURRENT FILING DATE: 1998-08-06
PRIOR APPLICATION NUMBER: 08/716,942
PRIOR FILING DATE: 1996-09-20
PRIOR FILING DATE: 1996-09-22
PRIOR FILING DATE: 1995-09-22
NUMBER OF SEQ ID NOS: 25
LENGTH: 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 22, Application US/09130337A Patent No. 6441148
                                         22:
                                                                                              TYPE: nucleic acid
STRANDEDNESS: DOUBLE
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                      318
61.00
45.74%
28.72%
2.55%
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                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                    HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Radomski, CCA APPLICANT: Seow, KT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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NAME/KEY:
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253 AlaGlnGluValTyrAspValThrGlyAlaGlyAspThrValIleGlyValLeuAlaAla 272
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                             FILING DATE: August 8, 1992
ATTORNEY/AGENT INFORMATION:
NAME: William P. Berridge
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 28835A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6400
TELEFAX: (703) 836-2787
INFORMATION FOR SEQ ID NO: 4:
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                     08/105,168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mycobacterium chitae
                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 268 base pairs
TYPE: nucleic acid
STRANDEDNESS: single-stranded
                                         FILING DATE: August 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR9210094
                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL:
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38.54%
26.04%
2.49%
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IDENTIFICATION METHOD:
OTHER INFORMATION:
PRIOR APPLICATION DATA:
                        APPLICATION NUMBER:
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CHROMOSOME/SEGMENT:
MAP POSITION:
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Best Local Similarity:
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ORIGINAL SOURCE:
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Patent No. 5849901
GENERAL INFORMATION:
APPLICANT: MABILAT et al.
TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET
TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET
TITLE OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
CARRESPONDENCE ADDRESS:
CARRESPONDENCE ADDRESS:
STREET: 700 South Washington Street, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 AlaGlnGluValTyrAspValThrGlyAlaGlyAspThrValIleGlyValLeuAlaAla 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            333 AlaAlaAlaArgLysArgGlyGluLysValValMetThrAsnGlyVal 348
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-912-020-325 (1-477) x US-08-105-168B-4 (1-268)
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FILING DATE: August 16, 1996
CLASSIFICATION: 536
                                                                                       ORIGINAL SOURCE:
ORGANISM: Mycobacterium chitae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: MS DOS 3.1
                   MOLECULE TYPE: DNA (genomic)
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" DS/HD
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                      DENTIFICATION METHOD:
COTHER INFORMATION:
US-08-105-168B-4
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                                                                                                                                      STRAIN:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                       POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Alexandria,
STATE: Virginia
ZIP: 22314
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
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                                           HYPOTHETICAL:
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                                                                      ANTI-SENSE
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TELECOMMUNICATION INFORMATION TELEPHONE: (206) 622-4900
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Washington
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Best Local Similarity:
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APPLICANT:
APPLICANT:
APPLICANT:
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CITY: Se
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         APPLICANT: GOLGOL, STEPHEN
APPLICANT: GOLGOL, STEPHEN
TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLECTIDE OF INTEREST FROM
TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
FILE REFERENCE: 3495-0169
CURRENT PAPPLICATION NUMBER: US/09/060,756
CURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 209
LENGTH: 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTAGTTGGGGGGGGGGGGCGGACTTCGCCGATTATCGCGACTGGCTGAAAGCCCGC--- 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 37, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Olllon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Unoghton, Raymond
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardisk, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 LeuSerLysSerLeuAlaAspValAşnValLysCysAspPheValSerVal 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----GGTGTCAACTGCGACCACGTTCTGATC 78
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6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-912-020-325 (1-477) x US-09-060-756-209 (1-236)
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-060-756-209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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38.60%
35.09%
2.47%
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Washington
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                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                            290 GTCACCGCCGTCACCACCACGACGCCGGTCGCGCTCTGAGTGCCGCC-----
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APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 148
                                                                                                                                                                                                                  290
24
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ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                    Length:
Matches:
Conservative:
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Indels:
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NAME: Maki, David J.
RECISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 CGCGCCGCCAAGACCGCCGTTGCCGCC 135
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APPLICATION NUMBER: US/08/818,111
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SYSTEM: PC-DOS/MS-DOS
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Sequence 37, Application US/08818111
Patent No. 6338852
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Dillon, Davin C.
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
TELEFAX: (206) 682-603 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                        58.50
42.03%
34.78%
2.44%
                                                                LENGRYH: 290 base pairs;
TYPE: nucleic acid
STRANDEDNESS: single
COS-08-818-112-37
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TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 ---GCCAATNCCGCC-------CTGGCCACCTTACGCC 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: DALLON, DAVID C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DATOR PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                              Conservative:
                                                                                                                                                                                                                                                                                                                                                                                     US-09-912-020-325 (1-477) x US-09-056-556-37 (1-290)
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Indels:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326 GluGluLeuLysLeuAlaValAlaAla 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 37, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Skeiky, Yasir A.W.
Dillon, Davin C.
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
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COUNTRY: USA
ZIP: 98104-7092
       linear
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Best Local Similarity:
Query Match:
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US-09-056-556-37
                                                                                                       Alignment Scores:
Pred. No.:
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                                                                                                                                                                                 Score:
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Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
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Matches:
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21017
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE GHARACTERISTICS:
LENGTH: 290 base pairs
TYPE: nucleic acid
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 37
SEQUENCE CHARACTERISTICS:
LENGTH: 290 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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Best Local Similarity:
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US-08-818-111-37
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No.:
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Percent Similarity:
 US-08-818-112-39
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                                                                                                                                                                                                                                                                    306 IleGluLeuGluAsnAlaValArgGlyArgAlaAspThrGlyPheGlyValMetThrGlu 325
                                                                                                                                                                                                                                                                                                                       286 PhealaasnalaalaalaGlyValValValGlyLysLeuGlyThrSerThrValSerPro 305
                                                                                                                                                                                                                                                                                                                                             206 GTTGCCACCGACCGCCGTCGGGGGGTTGCCTCCGCC------ACCGCC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-net, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Veardzik, Thomas S.
APPLICANT: Veardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: ELBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FLING DATE: 13 MAR-1997
CLASSIFICATION: 424
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6300 Columbia Center, 701 Fifth Avenue
                                                                                            Matches:
Conservative:
Mismatches:
Indels:
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                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Mak1, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 CGCGCCGCCAAGACCGCCGTTGCCGCC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326 GluGluLeuLysLeuAlaValAlaAla 334
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Patent No. 6290969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                      58.50
42.03%
34.78%
2.44%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 155 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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TOPOLOGY: linear
                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
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                                                    Alignment Scores:
       us-09-072-596-37
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CITY: Se
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                                                                          Pred. No.:
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TUBERCULOSIS
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                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 148
CORRESPONDENCE SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                  155
15
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18
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15
7
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
                                                        Conservative:
Mismatches:
Indels:
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                                                                                                                                                            US-09-912-020-325 (1-477) x US-08-818-112-39 (1-155)
                  Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 39, Application US/08818111
Patent No. 6338852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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57.50
53.66%
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LENGTH: 155 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Seattle
STATE: Washington
COUNTRY: USA
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                                                      Percent Similarity:
Best Local Similarity:
Query Match:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
US-08-818-111-39/c
                                                                                                                                                                                                                                                                                                                                                               302 Thr 302
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Alignment Scores:
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TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263 GlyAspThrValIleGlyValLeuAlaAlaThrLeu---AlaAlaGlyAsnSerLeuGlu 281
 282 GlualaCysPhePheAlaAsnAlaAlaAlaGlyValValValGlyLysSLeuGlyThrSer 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  æ
                      APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardalk, Daniel R.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
WUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Washington
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Mismatches:
Indels:
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NAME: Maki, David J
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPOTER READBLE FORM:
BUDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                            Sequence 39, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-MAY-1998
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Query Match:
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                                                                                                                                            RESULT 15
US-09-072-596-39/c
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                                                                                                         263 GlyAspThrValIleGlyValLeuAlaAlaThrLeu---AlaAlaGlyAsnSerLeuGlu 281
                                                                                                                               127 GGGGATACGACGGTGCCATTGTTCGACTCCGGCGTGCCGGGGGTGCTGGCGGG 68
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US-09-056-556-39/C
Sequence 39, Application US/09056556
Fatent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND WIMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                            155
15
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18
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                     US-09-912-020-325 (1-477) x US-08-818-111-39 (1-155)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-912-020-325 (1-477) x US-09-056-556-39 (1-155)
Mismatches:
Indels:
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21012
RELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.50
53.66%
36.59%
2.40%
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TYPE: nucleic acid
 36.59%
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Best Local Similarity:
Query Match:
 Best Local Similarity:
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Search completed: November 25, 2002, 01:01:12 Job time : 76 secs

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Sequence 90, Appl Sequence 159, App Sequence 159, App Sequence 2532, App Sequence 2560, App Sequence 2568, App Sequence 27168, App Sequence 27168, App Sequence 27168, App Sequence 27168, App Sequence 2729, App
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Sequence 1291, Ap
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23
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APPLICANT: Porsyth, R. Allyn
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
TITLE OF INVENTION: Genes identified as required for TITLE OF INVENTION: proliferation of E. coli
FILE REFERENCE: ELITARA.009A;
CURRENT APPLICATION NUMBER: US/09/741,669
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/173005
PRIOR FILING DATE: 1999-12-23
US-09-294-093B-4387
US-09-878-574-13727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 89, Application US/09741669 Patent No. US20020022718A1
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US-09-741-669-89
 Percent Similarity:
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LENGTH: 272
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Sequence 1264, Ap
Sequence 5061, Ap
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2377.031 Million cell updates/sec
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2393
I MKVTLPEFERAGVMVVGDVM......FEDGCSTINIIKKIQQDKKG 477
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                                                                                                                       November 24, 2002, 23:21:10 ; Search time 76 Seconds
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/cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/prodata/1/pubpna/USO6_NEW_PUB.seq:*
/cgn2_6/prodata/1/pubpna/USO6_PUBCOMB.seq:*
/cgn2_6/prodata/1/pubpna/USO6_PUBCOMB.seq:*
/cgn2_6/prodata/1/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/prodata/1/pubpna/USO8_PUBCOMB.seq:*
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                  GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                      nucleic search, using frame_plus_p2n model
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US-09-917-800A-1264
US-09-294-093B-5061
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published_Applications_NA:*
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 300
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: POTLET, MATK
APPLICANT: POTLET, MATK
APPLICANT: Constle, Arthur
APPLICANT: Castle, Arthur
APPLICANT: Castle, Arthur
APPLICANT: Castle, Arthur
APPLICANT: Castle, Arthur
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: MODICULAR TOXICOLOGY MODELING
FILE REFERENCE: 44921-5038-US
CURRENT FILING DATE: 2001-07-31
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-11-02
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/220, 645
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/290, 645
PRIOR FILING DATE: 2001-06-16
PRIOR APPLICATION NUMBER: US 60/290, 645
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/290, 645
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/290, 884
PRIOR APPLICATION NUMBER: US 60/290, 884
PRIOR APPLICATION NUMBER: US 60/290, 884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/290, 884
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                 US-09-912-020-325 (1-477) x US-09-741-669-89 (1-272)
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1264, Application US/09917800A

; Patent No. US20020119462Al

; GENERAL INFORMATION:

; APPLICANT: Mendrick, Donna
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112.00
54.93%
40.85%
4.68%
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100.00%
                                                                                                                                                                                                                                                                                                                                                       211 AAAAAAGGC 203
Best Local Similarity:
                                                                                                                                                                                                                                                                                                475 LysLysGly 477
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-09-917-800A-1264/c
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                              Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
TILEO FOR INVENTION: POLYNCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL FILLE REFERENCE: PL-0009 US
CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT APPLICATION NUMBER: 06/082,567
PRIOR APPLICATION NUMBER: 06/082,567
PRIOR APPLICATION NUMBER: 06/082,567
PRIOR APPLICATION NUMBER: 06/082,567
PRIOR FILING DATE: APril 21, 1998
NUMBER OF SEQ ID NOS: 6207
SEC ID NO 5061
LENGTH: 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GGGCAGGCTCCTTCGCCAGGTGCTCGTGTTGTAGGTAGATGCAAGTTTGATCTTTTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GIGAAAAGICAAGCIAICICATANCCITCCAACIICICGCCGGAICAIGCAGIITICAAAI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333 AlaAlaAlaArgLysArgGlyGluLysValValMetThrAsnGlyValPheAspIleLeu 352
218 GIGGACACCACGGGIGCIGGIGACAGITITGIGGGAGCGCTIGCCITCIACCIGGCTIAC 159
                                               276 ---AlaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnAlaAlaAlaGlyValVal 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09
                                                                           158 TACCCAAGTCTGTCCTGGAAGAAATGCTCAAGAGATCTAATTCCATCGTGCGGTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GCTGACACTGATTTAAGTGTTGTCGTTGCTGAGAAGTCTGCAGAAATCAAATGATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   · LeuLysLeuAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature

CTHER INFORMATION: Incyte ID No. US20010051335A1 700355719H1

NAME/KEY: Unsure

LOCATION: 83, 257, 263, 278

COTHER INFORMATION: a, t, c, 9, or other

US-09-294-093B-5061
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27
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Mismatches:
Indels:
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                                                                                                                                            295 ValGlyLysLeuGlyThrSerThrValSerPro 305
                                                                                                                                                                                           98 GICCAGGCCACAGGAACACAGTCCTCTTATCCA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                           Sequence 5061, Application US/09294093B Patent No. US20010051335A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 GTATCTATGGACGACGNATCGANTCAG 267
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Sequence 10531, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         373 AlaValAsnSerAspAlaSerThrLys 381
                                                                                                                                                                                                                                                                                                                                                                   Lalgudi, Raghunath, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.000967
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43.82%
29.21%
4.49%
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: LAI
                                                                                                                                                                                                                                           RESULT 3
US-09-294-093B-5061
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Pred. No.:
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Wed Nov 27 08:37:02 2002

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Conservative:
Mismatches:
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                                                                                                                                                                                                  171 AACGACGTGCGATCCGACGGGATCAAC 197
                                                                                                                                                                    89 ValAsnValLysCysAspPheValSer 97
                                                                                                                                                                                                                                                                US-09-741-669-90/c
; Sequence 90, Application US/09741669
; Patent No. US20020022718A1
; GENERAL INFORMATION:
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100.00%
2.93%
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US-09-741-669-90
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ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc_feature
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Best Local Similarity:
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US-09-923-876-159
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US-00-878-574-8726

Sequence 8725, Application US/09878574

Sequence 8725, Application US/09878574

Sequence 8725, Application US/09878574

Sequence 8725, Application US/09878574

SEQUENCERT: Dynum, Joseph R.

APPLICANT: La Rosa, Thomas J.

APPLICANT: La Rosa, Thomas J.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(15401)B

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 09/333,535

PRIOR PLIING DATE: 1999-06-14

NUMBER OF SEQ ID NOS: 15775

SEQ ID NO 8726

LENGTH: 265

LENGTH: 265
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: NULLER Acid Molecules and Other Molecules Associated with TITLE OF INVENTION: UNULES.
FILE REFERENCE: 38-21(15401)B
FILE REFERENCE: 38-21(15401)B
CURRENT FPLING DATE: 2001-12-21
PRIOR PAPLICATION NUMBER: 09/333,535
PRIOR PAPLICATION NUMBER: 09/333,535
RIOR PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 10531
LENGTH: 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 CACTCAGATGAGACAGTGAGTGAGCATAGAGGAAATCACTATCCAATTATGCATCTGCAT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        355 GlyHisValSerTyrLeuAlaAsnAlaArgLysLeuGlyAspArgLeuIleValAlaVal 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  375 AsnSerAspAlaSerThrLysArgLeuLysGlyAspSerArgProValAsnProLeuGlu 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 GlnArgMetIleValLeuGlyAlaLeuGluAlaValAspTrpValVal 410
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                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 700966779H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701101576H1
US-09-878-574-8726
                                                                                                                                                                                                                                                                                                                                                                              0.046
92.00
58.938
39.298
3.84%
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82.50
61.22%
40.82%
3.45%
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
Pred. No.:
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Pred. No.:
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Sequence 159, Application US/09923876

Sequence 159, Application US/09923876

Patent No. US2002001395811

GENERAL INFORMATION:

APPLICANT: Lalqudi, Radhunath V.

APPLICANT: Annigaki, Laura Y. (Ito)

APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING

FILE REFERENCE: PL-0012-1 CON

CURRENT FILING DATE: 2001-08-06

PRIOR APPLICATION NUMBER: 09/298,329

PRIOR APPLICATION NUMBER: 60/298,329

PRIOR APPLICATION NUMBER: 60/085,331

PRIOR APPLICATION NUMBER: 60/085,331

PRIOR FILING DATE: 1998-05-05

NUMBER OF SEQ ID NOS: 6332

SOFTWARE: PERL PROGram
                                   51 CCGGGGGGCCCCCCCGCAACGTTGCCGTCGCGTCGCGAACGCGGCG 110
                                                                                                                                                                                   111 TTCGTCGGGAAGCTCGGCGACGACGTTCGGGCACATGCTGGCCCGAATCCTGAAGGAG 170
50 ProGlyGlyAla---AlaAsnValAlaMetAsnIleAlaSerLeuSlyAlaAsnAlaArg
                                                                                                                                 69 LeuValGlyLeuThrGlyIleAspAspAlaAlaAlaArgAlaLeuSerLysSerLeuAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Corsyth, R. Allyn
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Syskind, Judith W.
ATILE OF INVENTION: Genes identified as required for TITLE OF INVENTION: proliferation of E. coli
FILE REFERENCE: ELITRA 0009A
CURRENT APPLICATION NUMBER: US/09/741,669
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/173005
PRIOR FILING DATE: 1999-12-3
NUMBER OF SEQ ID NOS: 481
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Jiang, Yuqiu
APPLICANT: Harlocker, Su
APPLICANT: Secrist, Heat
APPLICANT: Wang, Aijun
APPLICANT: Stolk, John A
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Best Local Similarity:
Query Match:
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US-10-046-935-1960
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Sequence 3810, Application US/09294093B

Patent No. US2010051335A1

BERERL INFORMATION:
APPLICANT:
TICALGANT:
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
FILE REFERENCE: PL-0009 US
CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567

PRIOR PILICATION NUMBER: 60/082,567

PRIOR FILING DATE: 40-11 12, 1998

NUMBER OF SEQ ID NOS: 6207

SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                      246
                                                                                                                                                                                                                                                                                                                 264
                                                                                                                                                                                                                                                                                                                                    71 CCTGTGATCCTATTGCCC-----AAGGAGAAGCTTGTTGACACGCCAACGCTGGGAGAACGTTGTTGACACGACGAGGGGGAGAAACTTGTTGACAACGCCAACGCTGGGAGAAAGCTTGTTGACAACGCCAACGGTGAC
                                                                                                                                                                                                                                                                                                                                                                                           125 GCTTTCGTCGGAGGCTTTCTCTCTCGGCTGGTCCAGGGCAAGAGCATGCGTG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValalaalaalaargLysArgGly------GluLysValValMetThrAsnGly 347
                                                                                                                                                                                                                                                                                                                                                                         265 ThrValIleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGluGluAlaCys 284
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11 GTGATTACTCAAGGCGCTGATCCAGTGGTTGTTGCTGAGGATGGGAAGGTGAAAACGTTC
                                                                                                                                                                                                                                                                                                             247 -----LeuHisMetProThrGlnAlaGlnGluValTyrAspValThrGlyAlaGlyAsp
                                                                                                                                                                                                                                                   229 LeuValThrArgSerGluGlnGlyMetSerLeuLeuGlnProGlyLysAlaPro--
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No. US20020013958A1 700156451H1
                                                                                                                                                                                                                                                                                                                                                                                                                                     285 PhePheAlaAsnAlaAlaAlaGlyValValValGlyLysLeuGly 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 ACGCTGGTTGCTACGCCGCCAATGTTATCATCCAGGCCCCAGGT 229
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18
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33
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18
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.9
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                                                                                                           Length:
Matches:
Conservative:
                                                                                                                                                                                                                      US-09-912-020-325 (1-477) x US-09-923-876-159 (1-272)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
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Indels:
                                                                                                                                                           Mismatches:
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                                                or other
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; OTHER INFORMATION: Incyte ID
US-09-294-093B-3810
 Incyte ID
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67.50
45.28%
33.96%
2.82%
                                                                                                           17.7
69.00
48.00%
24.00%
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                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
 OTHER INFORMATION:
              NAME/KEY: unsure

LOCATION: 3

COTHER INFORMATION:

US-09-923-876-159
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ORGANISM: Zea mays
                                                                                              Alignment Scores:
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                                                                                                            Pred. No.:
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Molecules and Other Molecules Associated with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270 LeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnAla 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290 AlaAlaGlyValValValGlyLySLeuGlyThrSerThrValSerProIleGluLeuGlu 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 AsnAlaValArgGlyArgAlaAspThrGlyPheGlyValMetThrGluGluLeuLys 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            350 AspIleLeuHisAlaGlyHisValSerTyrLeuAlaAsnAlaArqLysLeuGlyAspArg 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----AAACTTGGAGATACG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 LeualaValalaalaalaArgLysArgGlyGluLysValValMetThrAsnGlyValPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 ATTGTAATGAGGCTT----AAACGATGGGAACGGAAGGAGTGTAAACCAAACAGCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Glycine max
CTHER INFORMATION: Clone ID: LIB3028-024-Q1-B1-A3
US-09-878-574-2532
                         244 GCTTTTGATCTGTTCCATGCTGGACACGTCGAGATATTA 282
348 ValPheAspIleLeuHisAlaGlyHisValSerTyrLeu 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
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Indels:
                                                                           US-09-878-574-2532

US-09-878-574-2532

Sequence 2532, Application US/09878574

PAPLICANT: BYTUM, JOSEPH R.

APPLICANT: BYTUM, JOSEPH R.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Nucleic Acid Molecules a TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(15401)

CURRENT APPLICATION NUMBER: US/09/878,574

CURRENT FILING DATE: 2001-12-21

PRIOR FILING DATE: 1999-06-14

SEQ ID NO 2532

LENGTH: 281

LENGTH: 281
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Matches:
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Secrist, Heather
Wang, Aijun
Stolk, John A.
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65.00
46.60%
26.21%
2.72%
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APPLICANT: Ito, Laura, Y.
APPLICANT: Sharman, Bradley, K.
TITLE OF INVENTION: POLYNCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL FILE REFERENCE: PL-0009 US
CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: April 21,1998
NUMBER OF SCO ID NOS: 6207
SOFTWARE: PERL PROGram
SCO ID NO 5568
LENGTH: 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 ATGGAATCCATGGTCCATGCAGACACAAGATCATTATTCTGAAGAAGCCAAAGCTGTCT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                           291 AlaGlyValValValGlyLysLeuGlyThrSerThrValSerProlleGluLeuGluAsn 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331 AlaValAlaAlaAlaArgLysArgGlyGluLysValValMetThrAsnGlyValPheAsp 350
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OTHER INFORMATION: Incyte ID No. US20010051335A1 700357413H1
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER FILE REFERENCE: 210121.5272.
CURRENT APPLICATION NUMBER: US/10/046,935
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 2239
SOFTWARE: PSASSEQ for Windows Version 4.0
SEQ ID NO 1960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAGAAGTGGTCCAGGGACAAAGTAGGACCCCCAGAATAAGTCCC---
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23
23
114
229
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Conservative:
Mismatches:
Indels:
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LOCATION: 18, 26, 235, 271
OTHER INFORMATION: a, t, c, g, or other
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24.47%
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                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-046-935-1960
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Best Local Similarity:
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ORGANISM: Zea mays
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Pred. No.:
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Sequence 27168, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 CCAATCAGCAGGGCCCTCGGGGAACCNCAGGGCAATCTCCTTATTAGCACTCTCAATGCT 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 LysLeuArgValLeuSerArgAsnGlnGlnLeuIleArgLeuAspPheGluGluGlyPhe 125
                                                                                                                                                                                                                                                                                                                                                                                           28 ProThrSerArgIle-----SerProGluAlaProValValLySValAsnThr 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 AsnAlaArgLeuValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLeuSerLysSer 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 IleGluGluArgProGlyGlyAlaAlaAsnValAlaMetAsnIleAlaSerLeuGlyAla
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                                                                                                                                                                                                                                                                                           US-09-912-020-325 (1-477) x US-09-294-093B-5568 (1-298)
                                                       Conservative:
                                                                                                Mismatches:
Indels:
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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64.00
37.50%
24.04%
2.67%
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                                                  Percent Similarity:
Best Local Similarity:
Query Match:
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268 110 123 0

Conservative: Mismatches: Indels: Gaps:

80.8 63.00 50.00% 28.26% 2.63%

Length: Matches:

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119 TIGGITCIAGGCAAGGGCATTGAAGACIGCGTGAGGGCAGGTICCIATCCCGCAAACGIT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274 LeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnAlaAlaAlaGlyVal
                                                                                                                  NAME/KEY: misc_feature

CTHER INFORMATION: Incyte ID No. US20020013958A1 700157457H1

NAME/KEY: UDBUILE

LOCATION: 44, 266

COTHER INFORMATION: a, t, c, g, or other

US-09-923-876-729
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-912-020-325 (1-477) x US-09-923-876-729 (1-268)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294 ValValGlyLysLeuGly 299
SEQ ID NO 729
LENGTH: 268
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-954-531-285
                                                                                                                                                                                                                                                                           Alignment Scores:
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LENGTH: 176
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Sequence 729, Application US/09923876

Patent No. US20020013958A1

GENERAL INFORMATION:

APPLICANT: Lalqudi, Raghunath V.

APPLICANT: Lalqudi, Raghunath V.

APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING

FILE REFERENCE: PL-0012-1 CON

CURRENT APPLICATION NUMBER: US/09/923,876

CURRENT FILING DATE: 1999-06-6

PRIOR FILING DATE: 1999-04-21

PRIOR FILING DATE: 1999-04-21

PRIOR FILING DATE: 1999-05-05

NUMBER OF SEQ ID NOS: 6332

SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 ValAsnThrIleGluGluArgProGlyGlyAlaAlaAsnValAlaMetAsnIleAlaSer 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------ArgLeuValGlyLeu 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 TIGGGAGIGAGCICTIGIGAGICACAGGIIGGGGCTICCCIGIGIAACCIGGIGAGGCIC 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 ThrGlyIleAsp-----AspAlaAlaArgAlaLeuSerLysSerLeuAlaAspVal 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 ACAGGAGTCCAATGGCTTAGAGTGGCAGATAGGGCCATGAGTCGGGCCATTGTCTCTGTG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 ArgTyrTrpTyrGlyProThrSerArgIleSerProGluAlaProValProValValLys 42
                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: MAP TO AL121760.4

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN HBLIOO, SIGNAL = 0.99

OTHER INFORMATION: SWISSPROT HIT: Q43075, EVALUE 1,40e+00

OTHER INFORMATION: NT HIT: U69097.1, EVALUE 5,50e-01
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: DS 001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 27168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-912-020-325 (1-477) x US-09-864-761-27168 (1-267)
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Matches:
Conservative:
Mismatches:
Indels:
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63.50
44.44%
28.40%
2.65%
                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-864-761-27168
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                                                                                                                                                                                                                                                                                                                                        FEATURE:
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Sequence 285, Application US/09954531

Sequence 285, Application US/09954531

Patent No. US20020165180A1

GENERAL INFORMATION:
APPLICANT: Weaver, Zoe
TITLE OF INVENTION: Gene Sets
TITLE OF INVENTION: Gene Sets
FILE REFERENCE: 689209-77

CURRENT FILING DATE: 2002-05-02

PRIOR APPLICATION NUMBER: US/60/233,133

PRIOR PILING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: US/60/234,009

PRIOR PILING DATE: 2000-09-20

PRIOR APPLICATION NUMBER: US/60/234,034

PRIOR PILING DATE: 2000-09-20

PRIOR PILING DATE: 2000-09-20

PRIOR PILING DATE: 2000-09-20

PRIOR PILING DATE: 2000-09-20

PRIOR PILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 1392

COURTING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 1392
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28
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.0
179 ATCATCCAGCGCCCGGGC 196
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45.10%
29.41%
2.55%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapiens
US-09-954-531-285
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-----TTGGCA 153
350 AspIleLeuHisAlaGlyHisValSerTyrLeuAlaAsnAlaArgLysLeuGlyAspArg 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265 ThrVallleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGluGluAlaCys 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 ProlleGluLeuGluAsnAlaValArgGlyArgAlaAspThrGlyPheGlyValMetThr 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GATTTGCCAATGCATAACAGGGTTTCAATTCATTAATGAAGGGACTCAATCGCCTAGA 62
                                                                                                                                                                                US-09-974-300-7643

Sequence 7643.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085. 500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR FILING DATE: 2001-10-05
PRIOR FILING DATE: 2001-03-27
NUMBER: OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7643
LENGTH: 234
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                      123 CTTGGACCGTGGAATTCACATTTCATATTCTTG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              390 ValAsnProLeuGluGlnArgMetIleValLeu 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126
60.50
46.48%
29.58%
2.53%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CORGANISM: Bacillus clausii
US-09-974-300-7643
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Best Local Similarity:
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